

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2001, 09:31:40 ; Search time 1961.35 Seconds
(Without alignments)
11553.396 Million cell updates/sec

Title: us-09-484-964-1

Perfect score: 1465
Sequence: 1 cgggaagagttgttaaccc.....gataatgcatgcagcc 1465

Scoring table: OLIGO-NUC
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 7733874588 residues

Word size : 50

Total number of hits satisfying chosen parameters: 29

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl: *
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2: gb_ba2:*
3: gb_ba3:*
4: gb_in1:*
5: gb_in2:*
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13: gb_pi2:*
14: gb_pi3:*
15: gb_pi4:*
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96: gb_pi12:*
97: gb_pi13:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 778 | 53.1 | 1017 | 97 | HSU38784 |
| 2 | 775 | 52.9 | 1223 | 97 | HSU61397 |
| 3 | 775 | 52.9 | 1227 | 91 | BC006462 |
| 4 | 679 | 46.3 | 816 | 97 | HSU67132 |
| 5 | 625 | 42.7 | 160939 | 76 | AC079354 |
| 6 | 620 | 42.3 | 1514 | 9 | AR087051 |
| 7 | 620 | 42.3 | 1514 | 97 | HSU63117 |
| 8 | 343 | 23.4 | 590 | 93 | HSSMT3C |
| | | | | | X99586 H.sapiens m |

| | | | | | | |
|----|-----|------|--------|----|----------|-------------|
| 9 | 284 | 19.4 | 372 | 9 | AX021844 | Sequence |
| 10 | 255 | 17.4 | 306 | 97 | HSU72722 | Human gap m |
| 11 | 150 | 10.2 | 155913 | 81 | AL513282 | Human sapi |
| 12 | 150 | 10.2 | 167440 | 80 | AL513282 | Human sapi |
| 13 | 98 | 6.7 | 106168 | 87 | AC011450 | Human sapi |
| 14 | 98 | 6.7 | 178733 | 73 | AC068786 | Human sapi |
| 15 | 97 | 6.6 | 181861 | 72 | AC064836 | Human sapi |
| 16 | 65 | 4.4 | 510 | 7 | AF242526 | Human sapi |
| 17 | 65 | 4.4 | 158519 | 89 | AL135926 | Human sapi |
| 18 | 62 | 4.2 | 1187 | 94 | AF033353 | Human sapi |
| 19 | 62 | 4.2 | 180821 | 68 | AC023974 | Human sapi |
| 20 | 62 | 4.2 | 205741 | 60 | AC008548 | Human sapi |
| 21 | 62 | 4.2 | 235411 | 76 | AC084066 | Human sapi |
| 22 | 58 | 4.0 | 124764 | 60 | AC008377 | Human sapi |
| 23 | 58 | 4.0 | 146267 | 60 | AC008815 | Human sapi |
| 24 | 58 | 4.0 | 160970 | 61 | AC010501 | Human sapi |
| 25 | 58 | 4.0 | 161190 | 64 | AC016567 | Human sapi |
| 26 | 58 | 4.0 | 173048 | 67 | AC022142 | Human sapi |
| 27 | 58 | 4.0 | 173048 | 87 | AC008653 | Human sapi |
| 28 | 58 | 4.0 | 209022 | 71 | AC034212 | Human sapi |
| 29 | 52 | 3.5 | 162776 | 66 | AC021171 | Human sapi |

ALIGNMENTS

RESULT 1
LOCUS HSU38784 1017 bp mRNA
DEFINITION Human ubiquitin-like protein mRNA, complete cds.
ACCESSION U38784
VERSION U38784.1 GI:1574947
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1017)
AUTHORS Chen, Z., Pardington-Purtymun, P.E., Comeaux, J.C., Moyzis, R.K. and Ubel, D.J.
TITLE UBL1, a human ubiquitin-like protein associating with human RAD51/RAD52 proteins
JOURNAL Genomics, 36 (2), 271-279 (1996)
MEDLINE 96411684
REFERENCE 2 (bases 1 to 1017)
AUTHORS Shen, Z.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1995) Zhiyuan Shen, Life Sciences Division, Los Alamos National Lab, MS M888, Los Alamos, NM 87545, USA
FEATURES
source location/Qualifiers
1. 1017
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="This cDNA was cloned with the yeast two hybrid system. The protein interacts with human RAD51 and RAD52 proteins in yeast"
67. 372
/note="similar to ubiquitin and to yeast Smtp (suppressor of Mif2). Method: conceptual translation supplied by author"
/codon_start=1
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/translation="MSDQKAPKSTEDLDGKKEGYIKLVIGQSSSEHFVKKMTTLKKIKESYCOGQVPMNSRFLREGORIDNHTPKELGMEEDVLEIVQETGSHSTV"

BASE COUNT 310 a 180 c 213 g 314 t
ORIGIN

Query Match 53.1% Score 778; DB 97; Length 1017;
Best Local Similarity (99.9%) Pred. No. 0;
Matches 898; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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| DB | 119 | AAGTGGAATATTATTAACCTCAAGATGACAGATGAGTGGATTCCTCAAG | 178 |
| QY | 200 | tgaatagacacacatcctcaagaactcaagaatcactacgctcaagaaggtgttc | 259 |
| DB | 179 | TGAATAAGACACATCTCAAGAACTCAAGATCATACGTCAAGACGGGTGTC | 238 |
| QY | 260 | caatgaattacacacagttctcttgaaggtcagagaattgcataatcactca | 319 |
| DB | 239 | CAATGAATTAACCTCAAGATGAGTTCCTGAGGATTCCTGATATATATCTCA | 298 |
| QY | 320 | aagaactgggaatggagaagaagatgtagtgaattatcaagaacacaggggttc | 379 |
| DB | 299 | AAGAAGTGGGAATGAGGAAGAAGATGATGAGTGAAGTTATAGGACAAACGGGGGTC | 358 |
| QY | 380 | atcaacaggttagatattcttttttttttttttttttttttttttttttttt | 439 |
| DB | 359 | ATTCAACAGTTTAGATATCTTTTATTTTATTTTATTTTATTTTATTTTATTTT | 418 |
| QY | 440 | taaaaatgctcttcttgaatgctgctgctgctgctgctgctgctgctgctgct | 499 |
| DB | 419 | TAAATATGTTCTTTTATATGATGATGATGATGATGATGATGATGATGATGATG | 478 |
| QY | 500 | cttgaacacatctgtaatttgaatttgaatttgaatttgaatttgaatttgaatt | 559 |
| DB | 479 | CTTGAACATCTGTAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAATTT | 538 |
| QY | 560 | tgtgcgatttttggatgacagcctcagtcctcctcctcctcctcctcctcctcct | 619 |
| DB | 539 | TGTGCGATTTTGGTGAATCAAGCTCAGTCCCTTCATATATCCCTCTCTTTTAAA | 598 |
| QY | 620 | attaagtgtagcag | 679 |
| DB | 599 | ATTAGTGTCGACAG | 658 |
| QY | 680 | taataagatgac | 738 |
| DB | 659 | TAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG | 718 |
| QY | 739 | gcatttgatcttctcctcctcctcctcctcctcctcctcctcctcctcctcct | 798 |
| DB | 719 | GCATGTGATTTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT | 778 |
| QY | 799 | aactgaactgtggaagaaatgacacacacacacacacacacacacacacacac | 858 |
| DB | 779 | AACGTAACTGTGGAAGAAATGACCTTCTTCACTGCTGCTGCTGCTGCTGCTGCT | 838 |
| QY | 859 | ctggaac | 918 |
| DB | 839 | CTGACCAACAAAG | 898 |
| QY | 919 | tgaactactccaagaatgagcttcaatgagaagaagaagaagaagaagaagaaga | 978 |
| DB | 899 | TGACTACTCTCCAAAG | 958 |
| QY | 979 | tgtcagaagaatcccaagaagaatcctaatttcaatgagaagaagaagaagaaga | 1037 |
| DB | 959 | TGTCAGAAGATCCCAAGAAAGTTCTTAATTTTCAATTTGCAATTTAATTAATTA | 1017 |

RESULT 2
LOCUS HSU61397 1223 bp mRNA
DEFINITION Human ubiquitin-homology domain protein P101 mRNA, complete cds.
ACCESSION U61397
VERSION U61397.1 GI:1516693
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1223)

AUTHORS Boddly, M.N., Howe, K., Etkin, L.D., Solomon, E. and Freemont, P.S.
 TITLE PIC 1, a novel ubiquitin-like protein which interacts with the pML
 component of a multiprotein complex that is disrupted in acute
 promyelocytic Leukemia
 JOURNAL Oncogene 13 (5), 971-982 (1996)
 MEDLINE 96400311
 REFERENCE 2 (bases 1 to 1223)
 AUTHORS Howe, K., Boddly, M.N., Etkin, L.D., Solomon, E. and Freemont, P.S.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-1996) Somatic Cell Genetics, Imperial Cancer
 Research Fund, 44 Lincoln's Inn Fields, London WC2A 3PX, UK
 FEATURES
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 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

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 62 GAAGATTGTGTAACCCCGAGAGAGGTCTGTCTACCGAGCGCGTGTGCGGAGA 121
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 122 CCCCcgggttaagcaccgcatcatgtctgacgaggaagaaacccctcaagagac 181
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 242 GAGATTCACCTTCAAGTGAATGACACACATCTCAAGAACTCAAGATCAACTGT 301
 244 caagacagaggtgtccaatgaaatgaaatgaaatgaaatgaaatgaaatgaa 303
 302 CAAAGACAGGGGTGTCCAAATGAATTCACCTGAGGTCTTGTAGGGTCAAGAAATGCT 361
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 362 GATATATCTACTCCAAAGAACTGGGAATGAGAGAAATGTGATGAAATTTATCAG 421
 364 gaacaacaggggtgtcattcaacagtttagaatctcttattcttcttctccctc 423
 422 GAACAACAGGGGTGTCAACAGTTTGAATTTCTTTTATTTTCTTTTCCCTCC 481
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 482 AATCCTTTTATTTTAAATATGTTCTTTTGTAAATGTGTCTCAAAAGGAAATGGA 541
 484 aactgaccccatctcttgaacaacatcgttaattgaattcagtgctcattatcat 543
 542 AACTGACCCCATCTCTTGAACATCTGTAATTTGAATTTGATGCTCATTTATTCAT 601
 544 taattgttt 603
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Db 662 CCTCTCTTTTAAAAATTTACGTGTGCACAGAGAGTCACTTTTTCAGGACATTCATT 721
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 782 TGGCCCTATGTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 841
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RESULT 3
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 LOCUS Homo sapiens, ubiquitin-like 1 (sentrin), clone MGC:2095, mRNA,
 DEFINITION complete cds.
 ACCESSION BC006462
 VERSION BC006462.1 GI:13623670
 KEYWORDS MGC.
 SOURCE human.
 ORGANISM Homo sapiens
 Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1227)
 AUTHORS Strausberg, R.
 DIRECT SUBMISSION
 Submitted (09-APR-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov

Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 Info@gscc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Leticia Hsiao, Martin Krzyzinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McEavey, Steven
 Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stolt,
 Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/BLN at: <http://image.llnl.gov>
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 Location/Qualifiers

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 DB 48 GAAGGATTGTAAACCCGAGCGAGGTTCTGCTTACCCGAGCGCGCTGTGTGAGAGA 107
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 DB 108 CCCCcgggtgaagccacccgtcatcatgtctgaccagagagcaaacctcaactgagac 167
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 DB 168 TTGGGGATTAAGAAGAAGTGATATTAATTAACCTCAATGAGAGATAGCAGT 227
 QY 184 gggattcaactcaagaatgataacacacatctcaagaactcaagaactcaactgct 243
 DB 228 GAGATTCACTTCAAAAGTGAATGACACACATCTCAAGAACTCAAGAACTCAATCT 287
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 DB 288 CAAAGACAGGAGGTTCCATGATTCATCAAGGTTCTCTTGAAGGTCAGAAATTCCT 347
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 DB 408 GAACAACGGGGGTCAATCAACAGTTAGATATCTTTTATTTTCTTTCCCT 467
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 QY 483 aaactggaaccccatctcttgaacacatctgtaattgaattcagtgctcatattca 542
 DB 528 AAACAGGACCCCATCTCTTGAAGAACATCTGTATTTGAATTTCTAGTCTCATATTCA 587
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 QY 902 agataagtgagagtaatgactaactccaagaatggtcttcaactgagaagaagcatlta 961
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RESULT 4
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 LOCUS
 DEFINITION Human ubiquitin-related protein SUMO-1 mRNA, complete cds.
 ACCESSION U67122
 VERSION U67122.1 GI:1762972
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 816)
 Mahajan R., Delphin C., Guan T., Gerace L. and Melchior F.
 A small ubiquitin-related polypeptide involved in targeting RanGAP1
 to nuclear pore complex protein RanBP2
 Cell 88 (1), 97-107 (1997)
 97148692
 2 (bases 1 to 816)
 Mahajan R., Guan T., Delphin C., Gerace L. and Melchior F.
 Direct Submission
 Submitted (16-AUG-1996) Department of Cell Biology, The Scripps
 Research Institute, 10666 N. Torrey Pines Road, La Jolla, CA 92037,
 USA

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

FEATURES
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 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE Consortium Clone ID: 49768, 51818, 199507"
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 ubiquitin-related protein; similar to UBL1 encoded by
 GenBank Accession Number U38784, P1C1 encoded by GenBank
 Accession Number U72722"
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 /protein_id="AAC5096.1"
 /db_xref="GI:1762973"
 /translation="MSDQKAPSTEDLGKKKEGYIKLVIGDSSSEIHFVKMTTHL
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Query Match 46.3%; Score 679; DB 97; Length 816;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 729; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

|||||
1 GATTGTAAACCCCGGAGCCAGGTTCTGCTTACCAGGCGCGTGGCTGGAGAGACCC 60
68 cgggtgaagccaccgcatcatcgtcaccaggaaggcaaaccttcaactgagacttg 127
|||||
61 CGGGGAAGCCACCGTCATCTGTCACAGGAGGCAAAACCTTCMACTGAGGACTTGG 120
128 gggataaagaacagggatataataactcaaatgacattgacagagatagatga 187
|||||
121 GGGATTAAGAGAGGTGAATATATTAACCTAAAGCATTTGGACAGAGATAGCAGT 180
188 ttcacttcaagtgaaatgacacacatctcaagaactcaagaatcaactgactg 247
181 TTCACCTCAAGTGAATGACACACATCTCAAGAACTCAAGAAATCATCTACTG 240
248 gacaggggttccaaatgaatcaactcaactggttcccttggagggtcaagattg 307
241 GACAGGGGTTCATCAATGATTCACACAGGTTCTCTTGAAGGTCAGAGAAATG 300
308 atcatactccaagaactggaatggaatggaagaagatgattgaaattatcaagg 367
301 ATCATACTCCAAAGAACTGGAATGAGAGAGAAAGATGATTTGAAGTTATCAG 360
368 aaacggggggtcattcaacagtttagatattcttatttttttttttttttttt 427
|||||
361 AAACGGGGGTCATTCACAGTGTAGATTTCTTTTATTTTCTTTTCTTTTCTT 420
428 cttttatttttaaaatagttcttggtaatgtggttcaaaagaaatgaaact 487
|||||
421 CTTTATTTATTTTAAATAAGTTCTTTTGTATATGTTGTTCAAAACGGAAT 480
488 ggcacccatctcttgaacaacatctgtaatttgaattcagtcataatcaatt 547
481 GGAACCCCATCTCTTTGAACAACATCTGTAATTTGAATCTAGTCTCATTTCA 540
548 gttgttttcaatgtgcgtaatttgggtatcaagctcagtcacccctcattcc 607
541 GTTGTGTTTCATGTCGCTGATTTTGGTATCAAGCCCTCAGTCCCTCATTT 600
608 tcccttttaaaatcagtggtgacagagagatcaccctttcaggaacatttca 667
601 TCCTTTTAAAAATTTACGTGTGCACAGAGAGTCACTTTTTCAGAGACATTC 660
668 ggccttgggtgataaataagatgcacaaatgcaagtgttcataatgactttc 727
661 GCGTGTGGTGAATAAATGAATGATGACCAATGCAAGTGTTCATATATGCT 720
728 cctgattgtc 737
721 CCTGATGTTC 730

```

```

RESULT 5
AC079354/c AC079354 160939 bp DNA HTG 01-SEP-2000
LOCUS Homo sapiens chromosome UNK clone RP11-1145F21, WORKING DRAFT
DEFINITION
SEQUENCE, 11 unordered pieces.
ACCESSION AC079354
VERSION AC079354.1 GI:9931967
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 160939)
AUTHORS Waterston,R.H.
JOURNAL The sequence of Homo sapiens clone
TITLE Unpublished
REFERENCE 2 (bases 1 to 160939)
AUTHORS Waterston,R.H.
JOURNAL Direct Submission
TITLE Submitted (28-AUG-2000) Genome Sequencing Center, Washington
JOURNAL University School of Medicine, 4444 Forest Park Parkway, St. Louis,

```

```

COMMENT
MO 63108, USA
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information -----
Center project name: H.NH1145F21
----- Summary Statistics -----
Sequencing vector: M13, 1008
Sequencing vector: plasmid: 0%
Chemistry: Dye-terminator Big Dye, 0% of reads
Chemistry: Dye-terminator Big Dye, 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 155115 bases at least Q40
Consensus quality: 156942 bases at least Q30
Consensus quality: 157858 bases at least Q20
Insert size: 159939; sum-of-contigs
Insert size: 159939; sum-of-contigs
Quality coverage: 5.28 in Q20 bases; sum-of-contigs
Quality coverage: 5.62 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1 10518: contig of 10518 bp in length
* 10519 10618: gap of unknown length
* 10619 21836: contig of 11218 bp in length
* 21837 21936: gap of unknown length
* 21937 35609: contig of 13673 bp in length
* 35610 35709: gap of unknown length
* 35710 50278: contig of 14569 bp in length
* 50279 50378: gap of unknown length
* 50379 55743: contig of 15365 bp in length
* 55744 65843: gap of unknown length
* 65844 83507: contig of 17664 bp in length
* 83508 83607: gap of unknown length
* 83608 105340: contig of 21732 bp in length
* 105340 105439: gap of unknown length
* 105440 143858: contig of 38419 bp in length
* 143859 143958: gap of unknown length
* 143959 147000: contig of 3042 bp in length
* 147001 147100: gap of unknown length
* 147101 151655: contig of 4555 bp in length
* 151656 151755: gap of unknown length
* 151756 160939: contig of 9184 bp in length.
*
location/Qualifiers
1.160939
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="UNK"
/clone="RP11-1145F21"
1.10518
/feature="assembly_name:Contig10"
10619.21836
/feature="assembly_name:Contig11"
21937.35609
/feature="assembly_name:Contig12"
vector_end:17
vector_side:right"
35710.50278
/feature="assembly_name:Contig13"
50379.65743
/feature="assembly_name:Contig14"
65844.83507
/feature="assembly_name:Contig15"
83608.105339
/feature="assembly_name:Contig16

```


HSU83117 1514 bp mRNA PRI 09-JAN-1997
 LOCUS Human sentrin mRNA, complete cds.
 DEFINITION U83117
 ACCESSION U83117
 VERSION U83117.1 GI:1769601
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1514)
 AUTHORS Okura,T., Gong,L., Kamitani,T., Wada,T., Okura,I., Wei,C.-F.,
 Chang,H.-M. and Yeh,E.T.H.
 TITLE Protection Against Fas/APO-1- and Tumor Necrosis Factor-Mediated
 Cell Death by a Novel Protein, Sentrin
 JOURNAL J. Immunol. 157(10), 4277-4281 (1996)
 REFERENCE 2 (bases 1 to 1514)
 AUTHORS Okura,T., Gong,L., Kamitani,T., Wada,T., Okura,I., Wei,C.-F.,
 Chang,H.-M. and Yeh,E.T.H.
 TITLE Direct Submission
 JOURNAL Submitted (23-DEC-1996) Division of Molecular Medicine, Department
 of Internal Medicine, and Cardiovascular Research Center, Institute
 of Molecular Medicine for the Prevention of Human Diseases, The
 University of Texas-Houston Health Science Center, 2121 W. Holcombe
 Blvd., Suite 900, Houston, TX 77030, USA
 FEATURES
 source 1. 1514
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /tissue_type="placenta"
 136..441
 /note="ubiquitin-like protein"
 /codon_start=1
 /product="sentrin"
 /protein_id="AA83999.1"
 /db_xref="GI:1769602"
 /translation="MSDQKAPSTEDLGKKEGEYIKLVIGDSSFIHFVKMTTHL
 KKIKESYCOBQGVPMNSLRFLFGORIDAHNHTPKELGMEEDVIEVYQETGHSIV"
 CDS
 BASE COUNT 462 a 256 c 314 g 482 t
 ORIGIN
 Query Match 42.3%; Score 620; DB 97; Length 1514;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

422 tcaatccctttttatatttaaaatagctctttgtatgtgtgttcacaaacgaattg 481
 |||||||
 Db 470 TCAATCCCTTTTATTTTAAATAAGTCTTTGTATGATGGGTTCAAAGGAATG 529
 |||||||
 Oy 482 aaactgaccccaatctcttgaacatctgtaattgaattcagtcataatc 541
 |||||||
 Db 530 AAACTGCACCCCACTCTTTGAACAATCTGTGAATTTGAATTCATGATATTC 589
 |||||||
 Oy 542 atattgtgttttcaatgtgtcgtatctttgtatcaaacctcagtcctcatatc 601
 |||||||
 Db 590 ATATTGTTGTTTTCATGTGCTGATTTTGTGATCAGCTCAGTCCCTTCATATT 649
 |||||||
 Oy 602 accctcctttttaaattacgtgtgcagagagagcttccattcagaacattga 661
 |||||||
 Db 650 ACCCTCCCTTTTAAATAATAGTGTGCAAGAGTCACTTTTCAGACATTGCA 709
 |||||||
 Oy 662 ttttcagagctt 672
 |||||||
 Db 710 TTTTCAGGCTT 720
 |||||||
 RESULT 8
 HSSMT3C 590 bp mRNA PRI 19-MAR-1997
 LOCUS H.sapiens mRNA for SMT3C protein.
 DEFINITION X99586
 ACCESSION X99586.1 GI:1770520
 VERSION SMT3C gene; suppressor; ubiquitin-like protein.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 590)
 AUTHORS Lapenta,V., Chiurazzi,P., van der Spek,P., Pizzuti,A., Hanaoka,F.
 and Brahe,C.
 TITLE SMT3A, a human homologue of the S. cerevisiae SMT3 gene, maps to
 chromosome 21qter and defines a novel gene family
 JOURNAL Genomics 40 (2), 362-366 (1997)
 MEDLINE 97237059
 REFERENCE 2 (bases 1 to 590)
 AUTHORS Chiurazzi,P.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUN-1996) P. Chiurazzi, Universita' Cattolica - Roma,
 Largo F. Vito 1, I-00168 Roma, ITALY
 ORIGIN
 BASE COUNT 168 a 113 c 126 g 170 t 13 others
 Query Match 23.4%; Score 343; DB 93; Length 590;
 Best Local Similarity 99.7%; Pred. No. 2.9e-161;
 Matches 393; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | |
|------------|---|
| OY | 388 gtttag 393 |
| | |
| Db | 301 GTTTAG 306 |
| RESULT | 11 |
| AL513282/c | |
| LOCUS | AL513282.5 |
| DEFINITION | Homo sapiens chromosome 1 clone RP11-179G5, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces. |
| ACCESSION | AL513282 |
| VERSION | AL513282.5 GI:1316204 |
| KEYWORDS | HTG; HTGS_PHASE1; HTGS_DRAFT. |
| SOURCE | human. |
| ORGANISM | Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. |
| REFERENCE | 1 (bases 1 to 155913) |
| AUTHORS | Pavitt,R. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (25-FEB-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk requests: clonerequests@sanger.ac.uk On Feb 28, 2001 this sequence version replaced gi:13161719. Genome Center |
| COMMENT | |

COMMENT

web site: <http://www.sanger.ac.uk>
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: ba115N23

Assembly program: XGAP4, Version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator; Epi-amersham; 16% of reads
Dye-terminator: Big Dye; 83% of reads
Consensus quality: 165078 bases at least Q40
Consensus quality: 165122 bases at least Q30
Consensus quality: 16518 bases at least Q20
Insert size: 166840; sum-of-conflicts
Insert size: 138972; 3.5% error; agarose-fp
Quality coverage: 6.32x in Q20 bases; sum-of-conflicts
Quality coverage: 8.08x in Q20 bases; agarose-fp

* This record is a working draft sequence. It currently
 * consists of 7 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

| FEATURES | 1 | 17992 | contig of | 17991 bp | in length |
|----------|--------|---------------------|-----------|-----------|-----------|
| * | 17992 | 18091: gap of | 100 bp | | |
| * | 18092 | 34810: contig of | 16713 bp | in length | |
| * | 34811 | 34910: gap of | 100 bp | | |
| * | 34911 | 125180: contig of | 90270 bp | in length | |
| * | 125181 | 125280: gap of | 100 bp | | |
| * | 12581 | 129032: contig of | 3752 bp | in length | |
| * | 129033 | 129132: gap of | 100 bp | | |
| * | 129133 | 132599: contig of | 3467 bp | in length | |
| * | 132600 | 133699: gap of | 100 bp | | |
| * | 132700 | 141603: contig of | 8904 bp | in length | |
| * | 141604 | 141703: gap of | 100 bp | | |
| * | 141704 | 167440: contig of | 25737 bp | in length | |
| | | Location/Qualifiers | | | |

```
misc_feature
1. 17991
/note="assembly_fragment:00134
fragment_chain:1"
18092. 34810
/note="assembly_fragment:02111
fragment_chain:1"
34911. 125180
/note="assembly_fragment:03000
fragment_chain:1"
125281. 129032
/note="assembly_fragment:01240
fragment_chain:1"
129133. 13259
/note="assembly_fragment:00856
fragment_chain:1"
```

| | | | |
|--------------|---------|-------------------------------|---------------------------------|
| misc_feature | 132700, | .141603 | /note="assembly_fragment:00528" |
| misc_feature | 141704, | .167440 | /note="assembly_fragment:02701" |
| BASE COUNT | 47457 | a 37675 c 35802 g 45906 t 600 | others |
| ORIGIN | | | |

| | | | | |
|-----------------------|--------------|--------------------|---------------|----------------|
| Query Match | 10.2%; | Score 150; | DB 80; | Length 167440; |
| Best Local Similarity | 98.8%; | Pred. No. 4.1e-64; | | |
| Matches 400; | Conservative | 0; | Mismatches 5; | Indels 0; |
| | | | Gaps | 0 |

Dy 2/ gaagttcttctaaccgagcgccgtctgtcgtgcggagaagccccggcggtgaaggcacccatcat 86
|||
Db 154488 GAGGTTCTGCTTACCCGGAGCGCGTGCTGTGTCGAGAACCCGCCCGGGTGAAGCCACTGTCAT 154422

| | | | |
|----|--------|---|--------|
| QY | 147 | atatattaactcaaaagtcattgacgaagaatagcagatqagattcacccttgcanaatgaaaat | 206 |
| Db | 154428 | CATGCTTGACCAGGAGGCCAAAACCTTCAACTGAGGACTTTGGGGATTAAGAAGMAAGGTGA | 154369 |

QY 207 gacacacatctcaagaactcaagaatcatactgtcaagaagcgttccaatgaa 266
|||||
Db 154308 GACACACATCTCCTCAAGAACTCAAGAATCATATACTGTCAAGAAGCGTTCCCAATGAA 154309

Db 154248 TTCATTCAAGTTCTCTTTGAGGGTCAGAGAAATGCTGATATATCATCTACCTCCAAAAGAACT 154189

Db 154188 GGGAAATGAGGAAGAGATGTGATTGAAGTTTTCACGACAAATGGGGGCTCATTTCAAC 154129

RESULT 13
AC011450/C

| | | |
|------------|------------|--------------------|
| AC011450 | GI:7670120 | complete sequence. |
| AC011450.4 | GI:7670120 | |
| HTG. | | |
| KEYWORDS | | |
| VERSION | | |
| ACCESSION | | |
| NAME | | |

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 106168)

unpublished
2 (bases 1 to 106168)
DOE Joint Genome Institute.
Direct Submission

REFERENCE
AUTHORS
TITLE
JOURNAL
DOI

3 (bases 1 to 106168)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted

3 (bases 1 to 106168)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Submitted

On Apr 29, 2000 this sequence version replaced gi:7021594.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford University

Sequencing completed at Shanghai Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number Of Errors is 0.3.

SRS Content:

SHCC-34723 G28380
SHCC-58287 G38466.

FEATURES
Location/Qualifiers
1. 106168
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
/clone="CTC-30107"

BASE COUNT 26156 a 24429 c 24340 g 31243 t
ORIGIN

Query Match 6.7%; Score 98; DB 87; Length 106168;
Best Local Similarity 100.0%; Pred. No. 5.9e-38;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

275 ggttcctcttgaaggctcagagaattgctgatacactcaagaagactgggaatg 334
|||||
Db 74410 GGTTCCTCTTGAAGGCTCAGAGATTGCTGATATCATCTCAAAAGACTGGGAATGG 74351
|||||
QY 335 aggaagaagatgtgtatgaattatcaggaacaacg 372
|||||
Db 74350 AGGAAGAAGATGTGATTGAAGTTATCAGGAACAAACG 74313

RESULT 14

AC068786 178733 bp DNA HTG 08-MAR-2001
LOCUS Homo sapiens chromosome 19 clone RP11-50111, WORKING DRAFT
DEFINITION
SEQUENCE, 15 unordered pieces.

AC068786
AC068786.11 GI:13249431
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
human.
ORGANISM

REFERENCE
AUTHORS Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 178733)
Abola, A.P., Bruno, D., Conn, L., Dela Rosa, M., Faulkner, D.,
Pederspiel, N., Glukhov, S., Hansen, N., Herman, Z.S., Hyman, R.,
Mao, J., Lam, B., Marathe, R., Miranda, M., Morehouse, A.J., Nguyen, M.,
Oefner, P., Palm, C.J., Ramirez, D., Southwick, A.M., Wilhelmy, J.,
Yu, S. and Davis, R.W.

JOURNAL
REFERENCE
AUTHORS

TITLE
JOURNAL
Submitted (09-MAY-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
USA

COMMENT

On Mar 8, 2001 this sequence version replaced gi:13236646.
Center: Genome Center
Center: Stanford DNA Sequencing and Technology Development

Center code: SDSNDC
Web site: http://sequence-www.stanford.edu/group/human/
Contact: hum-info@sequence.stanford.edu
Project Information

Center project name: 899
Center clone name: RP11-50111
Center project name: 899

Sequencing Vector: M13mp18; X02513
Chemistry: Dye-terminator 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168546 bases at least Q40
Consensus quality: 171030 bases at least Q30
Consensus quality: 172366 bases at least Q20
Insert size: 178045; agarose-1p

FEATURES
Source

misc_feature
1726..3491
/note="assembly_name:Contig21"
1726..3491
/note="assembly_name:Contig24"
3592..5210
/note="assembly_name:Contig30"
5311..7665
/note="assembly_name:Contig32"
7766..11506
/note="assembly_name:Contig33"
11607..16778
/note="assembly_name:Contig34"
16879..24169
/note="assembly_name:Contig35"
24270..34333
/note="assembly_name:Contig36"
34434..46447
/note="assembly_name:Contig37"
46548..58761
/note="assembly_name:Contig38
clone_end:17
58862..73753
/note="assembly_name:Contig39"
73854..92184
/note="assembly_name:Contig40"
92285..114445

Insert size: 177333; sum-of-contigs
Quality coverage: 9.2x in Q20 bases; agarose-1p
Quality coverage: 9.2x in Q20 bases; sum-of-contigs.
NOTE: This is a 'working draft' sequence. It currently
consists of 15 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

1625: contig of 1625 bp in length
1725: gap of unknown length
1726: contig of 1766 bp in length
3491: gap of unknown length
3591: gap of unknown length
3592: contig of 1619 bp in length
5210: gap of unknown length
5310: gap of 2355 bp in length
5311: 7665: gap of unknown length
7666: 11506: contig of 3741 bp in length
7766: 11606: gap of unknown length
11507: 16778: contig of 5172 bp in length
11607: 16778: gap of unknown length
16779: 16878: gap of 7291 bp in length
16879: 24169: contig of 10064 bp in length
24170: 34333: gap of unknown length
34333: 34433: gap of unknown length
34433: 46447: contig of 12014 bp in length
46447: 46547: gap of unknown length
46547: 58761: contig of 12214 bp in length
58761: 58861: gap of unknown length
58861: 73753: contig of 14892 bp in length
73753: 73853: gap of unknown length
73853: 92184: contig of 18331 bp in length
92184: 92284: gap of unknown length
92284: 114445: gap of 22161 bp in length
114445: 114545: gap of unknown length
114545: 140410: contig of 25865 bp in length
140410: 140510: gap of unknown length
140510: 178733: contig of 38223 bp in length.
140511

```

/misc_feature      /note="assembly_name:Contig41
                   clone_end:SP6"
misc_feature      /note="assembly_name:Contig42"
                   /note="assembly_name:Contig43"
misc_feature      /note="assembly_name:Contig43"
BASE COUNT      50350 a 40923 c 42172 g 43887 t 1401 others
ORIGIN
Query Match      6.7%; Score 98; DB 73; Length 178733;
Best Local Similarity 100.0%; Pred. No. 5.9e-38;
Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 275 ggtctcttggagggcgaagattcgtatatactccaaagaactgggaatg 334
Db 120102 GGTTCCTTTAGGGCTCAGAGATTGCTGATATCATCTCCAAAAGAACTGGGAATGG 120161
QY 335 aggaagaagatgtgattgaattatcaaggaacaaacg 372
Db 120162 AGGAAGAAGATGTGATTGAATTATCAGACAAACG 120199

```

```

RESULT 15
AC064836/c
LOCUS      AC064836 181861 bp DNA HTG 17-AUG-2000
DEFINITION Homo sapiens chromosome 2 clone RP11-68606, WORKING DRAFT SEQUENCE,
             17 unordered pieces.
ACCESSION  AC064836
VERSION     AC064836.4 GI:9838313
KEYWORDS   HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            1 (bases 1 to 181861)
            Waterston,R.H.
            The sequence of Homo sapiens clone
            Unpublished
            2 (bases 1 to 181861)
            Waterston,R.H.
            Direct Submission
            Submitted (22-APR-2000) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
            On Aug 17, 2000 this sequence version replaced gi:7801500.

```

```

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Project Information
Center project name: H_NH0686006
Summary Statistics
Sequencing vector: M13; 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 173047 bases at least Q40
Consensus quality: 176179 bases at least Q30
Consensus quality: 178311 bases at least Q20
Insert size: 191000; agarose-fp
Quality coverage: 5.14 in Q20 bases; agarose-fp
Quality coverage: 5.45 in Q20 bases; sum-of-coverage
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence

```

```

FEATURES
source
* as soon as it is available and the accession number will
* be preserved.
1       1669: contig of 1669 bp in length
1670    1770: gap of unknown length
1770    3011: contig of 1242 bp in length
3011    3112: gap of unknown length
3112    5912: contig of 2801 bp in length
5912    6013: gap of unknown length
6013    7803: contig of 1790 bp in length
7803    7902: gap of unknown length
7902    12401: contig of 4499 bp in length
12401   12501: gap of unknown length
12501   16034: gap of 3533 bp in length
16034   16135: gap of unknown length
16135   21575: contig of 5440 bp in length
21575   21675: gap of unknown length
21675   26187: contig of 4512 bp in length
26187   26287: gap of unknown length
26287   31932: contig of 5646 bp in length
31932   32032: gap of unknown length
32032   40012: contig of 7980 bp in length
40012   40113: gap of unknown length
40113   46865: contig of 6753 bp in length
46865   46966: gap of unknown length
46966   56137: contig of 9172 bp in length
56137   56238: gap of unknown length
56238   63975: contig of 7738 bp in length
63975   64075: gap of unknown length
64075   78167: contig of 14092 bp in length
78167   78267: gap of unknown length
78267   95028: contig of 16761 bp in length
95028   95128: gap of unknown length
95128   127606: contig of 32478 bp in length
127606  127707: gap of unknown length
127707  181861: contig of 54155 bp in length.
Location/Qualifiers
1. 181861
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-68606"
1. 1669
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1770. 3011
/note="assembly_name:Contig17"
3112. 5912
/note="assembly_name:Contig19"
6013. 7802
/note="assembly_name:Contig20"
7903. 12401
/note="assembly_name:Contig21"
12502. 16034
/note="assembly_name:Contig22"
16135. 21574
/note="assembly_name:Contig23"
21675. 26186
/note="assembly_name:Contig24"
26287. 31932
/note="assembly_name:Contig25"
32032. 40012
/note="assembly_name:Contig26"
40113. 46865
/note="assembly_name:Contig27"
46966. 56137
/note="assembly_name:Contig28"
56238. 63975
/note="assembly_name:Contig29
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vector_side:right"
64076. 78167
/note="assembly_name:Contig30
clone_end:SP6
vector_side:left"

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misc_feature      /note="assembly_name:Contig17"
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misc_feature      /note="assembly_name:Contig28"
misc_feature      /note="assembly_name:Contig29
clone_end:17
vector_side:right"
64076. 78167
/note="assembly_name:Contig30
clone_end:SP6
vector_side:left"

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Mon Aug 20 11:48:00 2001

us-09-484-964-1.01i.rge

Page 13

misc_feature 78268 .95028
/note="assembly_name:Contig31"
misc_feature 95129 .127606
/note="assembly_name:Contig32"
misc_feature 127707 .181861
/note="assembly_name:Contig33"
BASE COUNT 52240 a 39002 c 38693 g 50312 t 1614 others
ORIGIN

Query Match 6.6%; Score 97; DB 72; Length 181861;
Best Local Similarity 100.0%; Pred. No. 1.9e-37;
Matches 97; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 gaagatttgaaccccgagcgaggttctgtaccagagcgctgtgtgagagaga 63
|||||
DB 71306 GAAGATTGTTGTAACCCCGAGCGAGGTTCTGTACCCGAGGCCCTGCTGTGCGGAGA 71247
|||||
QY 64 ccccggtgaagccacgcatcatgtgtgacagag 100
|||||
DB 71246 CCCCCGGTGAAGCCACCGTCATCATGTGTGACCAAG 71210
|||||

Search completed: August 17, 2001, 11:25:44
Job time: 6844 sec

•
•
•

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2001, 09:34:05 ; Search time 84.61 Seconds
(without alignments)

3277.873 Million cell updates/sec

Title: US-09-484-964-1

Perfect score: 1465
Sequence: 1 cgggaagattgttaaaccc.....gataatggcagtcagcc 1465

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 324599 seqs, 94655562 residues

Word size : 50

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/6C.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/6dckfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-----------------|
| 1 | 620 | 42.3 | 1514 | 2 | US-09-213-768-1 |

ALIGNMENTS

Query Match 42.3% ; Score 620 ; DB 2 ; Length 1514;
Best Local Similarity 99.3% ; Pred. No. 4.2e-279;
Matches 670 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 2 | ggaagagattgttaaacccggagaggttcgtaccggagccgctgctgcgga | 61 |
| DB | 50 | gggaagattgttaaacccggagaggttcgtaccggagccgctgctgcgga | 109 |
| QY | 62 | gaccccggtgaaagccacgctcatctgtctgacagaggaacaccttcagag | 121 |
| DB | 110 | gaccccggtgaaagccacgctcatctgtctgacagaggaacacaccttcagag | 169 |
| QY | 122 | acttgggggataagaagcaggtgaatataataacccaagtcattggcaggataga | 181 |
| DB | 170 | acttgggggataagaagcaggtgaatataataacccaagtcattggcaggataga | 229 |
| QY | 182 | gtgagattcacttcaagtgaaatgacacacatctcaagaactcaagaatcact | 241 |
| DB | 230 | gtgagattcacttcaagtgaaatgacacacatctcaagaactcaagaatcact | 289 |
| QY | 242 | gtcaagacaggtgttccaatgaaatcactcaggttctcttggagggtcagaagt | 301 |
| DB | 290 | gtcaagacaggtgttccaatgaaatcactcaggttctcttggagggtcagaagt | 349 |
| QY | 302 | ctgataatcactcccaaaagacactgggaatggaggaagagatgttgaaattac | 361 |
| DB | 350 | ctgataatcactcccaaaagacactgggaatggaggaagagatgttgaaattac | 409 |
| QY | 362 | aggaacaaacgggggtcattcaacagtttagatatcttcttcttcttcc | 421 |
| DB | 410 | aggaacaaacgggggtcattcaacagtttagatatcttcttcttcttcc | 469 |
| QY | 422 | tcaatctttttatattttaaataagttcttcttgaatggtgttcaaaacggaatg | 481 |
| DB | 470 | tcaatctttttatattttaaataagttcttcttgaatggtgttcaaaacggaatg | 529 |
| QY | 482 | aaaactggcaccatctcttggaaacatctgttaatttgaattcagtcattatc | 541 |
| DB | 530 | aaaactggcaccatctcttggaaacatctgttaatttgaattcagtcattatc | 589 |
| QY | 542 | attatgtttgtttcattatgtctgatttttggatcaagccatgacctcatt | 601 |
| DB | 590 | attatgtttgtttcattatgtctgatttttggatcaagccatgacctcatt | 649 |
| QY | 602 | acccttcctttttaaataaatacgtgacagagaggtcacccttttcaggaattga | 661 |
| DB | 650 | acccttcctttttaaataaatacgtgacagagaggtcacccttttcaggaattga | 709 |
| QY | 662 | ttttcaggctt 672 | |
| DB | 710 | ttttcaggctt 720 | |

Search completed: August 17, 2001, 11:20:01
Job time: 6356 sec

RESULT 1
US-09-213-768-1
; Sequence 1, Application US/09213768
; Patent No. 5985664
; GENERAL INFORMATION:
; APPLICANT: Brenda F. Baker
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF SENTRIN EXPRESSION
; FILE REFERENCE: RTS-0026
; CURRENT APPLICATION NUMBER: US/09/213, 768
; CURRENT FILING DATE: 1998-12-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (136)..(441)
US-09-213-768-1

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OM nucleic - nucleic search, using sw model

Run on: August 17, 2001, 10:09:15 ; Search time 131.18 Seconds
(without alignments)
7012.318 Million cell updates/sec

Title: US-09-484-964-1

Perfect score: 1465
Sequence: 1 cgggaagattgttaaaccc.....gataatggcatgcacgc 1465

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 730101 seqs, 313950809 residues

Word size : 50

Total number of hits satisfying chosen parameters: 9

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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1: /SIDSI/gcgdata/geneseq/geneseq/NA1980.DAT.*
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7: /SIDSI/gcgdata/geneseq/geneseq/NA1986.DAT.*
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21: /SIDSI/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 1465 | 100.0 | 1465 | 19 | AAV34564 |
| 2 | 895 | 61.1 | 1196 | 19 | AAV59722 |
| 3 | 895 | 61.1 | 1220 | 19 | AAV59557 |
| 4 | 620 | 42.3 | 1514 | 21 | AA35859 |
| 5 | 300 | 20.5 | 616 | 21 | AA16215 |
| 6 | 284 | 19.4 | 372 | 18 | AA63339 |
| 7 | 284 | 19.4 | 372 | 22 | AA59399 |
| 8 | 197 | 13.4 | 425 | 17 | AA703735 |
| 9 | 85 | 5.8 | 180 | 16 | AA119668 |

ALIGNMENTS

| | |
|--------|---|
| RESULT | 1 |
| ID | AAV34564 |
| AC | AAV34564 standard; DNA; 1465 BP. |
| XX | |
| XX | AAV34564: |
| XX | |
| XX | 11-SEP-1998 (first entry) |
| XX | |
| XX | Homo sapiens sentrin-1 gene. |
| XX | |
| XX | sentrin-1; protection; tumour necrosis factor; tnfi; apoptosis; |
| KW | Fas/Apo-Induced; tumour cell death; induction; tumour aggressiveness; |
| KW | detection; determination; ss. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| XX | Key |
| XX | Location/Qualifiers |
| FT | 88..393 |
| FT | /*tag= a |
| FT | /product= sentrin-1 polypeptide |
| XX | |
| XX | MO9820038-AL. |
| XX | |
| XX | 14-MAY-1998. |
| XX | |
| XX | 05-NOV-1997; 97WO-US20344. |
| XX | |
| XX | 05-NOV-1996; 96US-0030302. |
| XX | |
| XX | (TEXA) UNIV TEXAS SYSTEM. |
| XX | |
| XX | Yeh ETH; |
| XX | PI |
| XX | |
| DR | WPI: 1998-286868/25. |
| DR | P-PSDB; AAM60079. |
| XX | |
| PT | New isolated sentrin polypeptide(s) - which inhibit TNF receptor or |
| PT | Fas/Apo-Induced apoptosis, used to develop products for inducing |
| PT | cell death in tumours |
| XX | |
| PS | Claim 10; Page 76-77; 120pp; English. |
| XX | |
| CC | The sequence is that encoding the sentrin-1 polypeptide. |
| CC | Sentin polypeptides have the ability to protect or guard |
| CC | cells from tumour necrosis factor (TNF) or Fas/Apo induced |
| CC | cell death (apoptosis). Inhibitors of the sentrin polypeptides, |
| CC | e.g. antibodies, can be used for inducing cell death. |
| CC | particularly in tumours. The products can also be used for |
| CC | determining the aggressiveness of a tumour and for detection and |
| CC | isolation of products. The sentrin polypeptide can also be used to |
| CC | detect a ubiquitin conjugating enzyme polypeptide or PML polypeptide. |
| XX | |
| SQ | Sequence 1465 BP; 455 A; 248 C; 292 G; 470 T; 0 other; |

Query Match 100.0%; Score 1465; DB 19; Length 1465;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1465; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | |
|----|-----|---|
| QY | 1 | cgggaagattgttaaaccccgagaggttctgttaccgagcgctgtgag 60 |
| DB | 1 | cgggaagattgttaaaccccgagaggttctgttaccgagcgctgtgag 60 |
| QY | 61 | agaccgggtgaagccacgcgtatcatgtctgacgaaggaagcaacttaactgag 120 |
| DB | 61 | agaccgggtgaagccacgcgtatcatgtctgacgaaggaagcaacttaactgag 120 |
| QY | 121 | gacttggggaataaggaaggtgaatatataactcaagtcattgtgacaggtatgc 180 |
| DB | 121 | gacttggggaataaggaaggtgaatatataactcaagtcattgtgacaggtatgc 180 |

QY 181 agtgaattccttcaaaagtgaataatgacaacacatctcaagaaactcaagaatcac 240
| | | | |
Db 181 agtgaattccttcaaaagtgaataatgacaacacatctcaagaaactcaagaatcac 240
QY 241 tgcataagacagggtgttcccaatgaattcaatcaggttctcttgagggtcagaagatt 300
| | | | |
Db 241 tgcataagacagggtgttcccaatgaattcaatcaggttctcttgagggtcagaagatt 300
QY 301 gctataatcaatcctcaaaaagaacatggaatggaagaagaatgattgattgaattat 360
| | | | |
Db 301 gctataatcaatcctcaaaaagaacatggaatggaagaagaatgattgattgaattat 360
QY 361 caaggaacaacagggggttcattcaacagttatagattctctttatctttctttcttcc 420
| | | | |
Db 361 caaggaacaacagggggttcattcaacagttatagattctctttatctttctttcttcc 420
QY 421 ctcaatcctttttatttttaaaaaatagttcttttgaatgtgtgttcaaaagggaatt 480
| | | | |
Db 421 ctcaatcctttttatttttaaaaaatagttcttttgaatgtgtgttcaaaagggaatt 480
QY 481 gaaaactgaccccatctcttgaaacatctgtaattgtaatttgaattgattgattgatt 540
| | | | |
Db 481 gaaaactgaccccatctcttgaaacatctgtaattgtaatttgaattgattgattgatt 540
QY 541 cattattgtttgttttcaatgtgtgatttttggatcaagcctcagtccttcattat 600
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Db 541 cattattgtttgttttcaatgtgtgatttttggatcaagcctcagtccttcattat 600
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| | | | |
Db 601 taccctctcttttttaaaaattacggtgacacagagaaggttcaccttttcaagaacatgac 660
QY 661 atttcaagcgtgtgtgtgaataaataagacacagacatgaaatgttcaataagacttcc 720
| | | | |
Db 661 atttcaagcgtgtgtgtgaataaataagacacagacatgaaatgttcaataagacttcc 720
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| | | | |
Db 721 aattggcctgtgtgttcaacatgtgatttcttcaactcctgacgtgacattcaattgga 780
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| | | | |
Db 781 gatggaagttttcagagacatgaaatgtgaaatgacacttcttcaacttgaagacta 840
QY 841 ctttaaaatttgaaggtctggaacacaaagaagaatatacaggttgaagtcagaatga 900
| | | | |
Db 841 ctttaaaatttgaaggtctggaacacaaagaagaatatacaggttgaagtcagaatga 900
QY 901 cagataaggtggaataatgactaactcaaaagatggttcaactgaaagaagaagcatttt 960
| | | | |
Db 901 cagataaggtggaataatgactaactcaaaagatggttcaactgaaagaagaagcatttt 960
QY 961 aagattttttaaanaacttctgcagaagaatcccaagaagaatcttaatttcaatgaacatt 1020
| | | | |
Db 961 aagattttttaaanaacttctgcagaagaatcccaagaagaatcttaatttcaatgaacatt 1020
QY 1021 aataaagctataactgacgaataatatacaacacacacatgctctttttagatttatt 1080
| | | | |
Db 1021 aataaagctataactgacgaataatatacaacacacacatgctctttttagatttatt 1080
QY 1081 gtacttttggcccggaataggttttaaatggaatcttcttaccacatttataaa 1140
| | | | |
Db 1081 gtacttttggcccggaataggttttaaatggaatcttcttaccacatttataaa 1140
QY 1141 ataaacataatttgcataaaatcgtactaatttatttattttaaattgcatagaaga 1200
| | | | |
Db 1141 ataaacataatttgcataaaatcgtactaatttatttattttaaattgcatagaaga 1200
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| | | | |
Db 1201 aaaaaatgctaaataaagggttctctgcaataaataatggaatgacatggtacaat 1260

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Db 1261 ttttctcattactgtacagggaatgtttaatgactttggagcactgaaagtactga 1320
QY 1321 agtgccttgcatacaaggatttaataaggccacaataccttttaatactcagtttc 1380
| | | | |
Db 1321 agtgccttgcatacaaggatttaataaggccacaataccttttaatactcagtttc 1380
QY 1381 tgtttttttaaacttgatatatccgtatgtgtcatatttgaatacaggtacccaatca 1440
| | | | |
Db 1381 tgtttttttaaacttgatatatccgtatgtgtcatatttgaatacaggtacccaatca 1440
QY 1441 tgttgataaatgtggcatgacagcc 1465
| | | | |
Db 1441 tgttgataaatgtggcatgacagcc 1465

RESULT 2
AAV59722
ID AAV59722 standard; DNA; 1196 BP.
XX
AC AAV59722;
XX
DT 19-JAN-1999 (first entry)
XX
DE Human secreted protein gene 47 clone HOGAV75.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukemia;
developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;
cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WC9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98MO-US04493.
XX
PR 02-OCT-1997; 97US-006160.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047504.
PR 23-MAY-1997; 97US-0047581.

| | | |
|----|---|---|
| | XX | PI Bednarik DP, Brewer LA, Carter KC, Duan R, Edner R, Endress GA; |
| | XX | Pi Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS; |
| | XX | PI Kyaw H, Laifuer DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA; |
| | XX | Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z; |
| | DR | WPI: 1998-506364/43. |
| | DR | P-PSSDB; AAW74938. |
| | XX | PT New isolated human genes and the secreted polypeptide(s) they encode |
| | PT | - useful for diagnosis and treatment of e.g. cancers, neurological |
| | PT | disorders, immune diseases, inflammation or blood disorders |
| | PS | Claim 1; Page 449; 721pp; English. |
| | XX | This sequence represents a nucleic acid molecule designated Gene 47 from |
| | CC | the human cDNA clone HO6AV75 (deposited as clone ATCC 97897 and ATCC |
| | CC | 209043) which encodes a secreted human protein. The gene can be used to |
| | CC | generate fusion proteins by linking to the gene to a human |
| | CC | immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of |
| | CC | the fused protein as compared to the human protein only. |
| | CC | The invention relates to 186 novel genes and their fragments (nucleic |
| | CC | acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026) |
| | CC | which are useful for preventing, treating or ameliorating medical |
| | CC | conditions e.g. by protein or gene therapy. Also, pathological |
| | CC | conditions can be diagnosed by determining the amount of the new |
| | CC | polypeptides in a sample or by determining the presence of mutations in |
| | CC | the new polynucleotides. Specific uses are described for each of the 186 |
| | CC | polynucleotides, based on which tissues they are most highly expressed in |
| | CC | (see AAV59511 for described uses). |
| | XX | |
| | SO | Sequence 1196 BP; 360 A; 212 C; 259 G; 364 T; 1 other; |
| | Query Match | 61.1%; Score 895; DB 19; Length 1196; |
| | Best Local Similarity | 99.8%; Pred. No. 0; |
| | Matches 1065; Conservative | 0; Mismatches 1; Indels 1; Gaps 1 |
| OY | 4 gaagatttgaaaaccccgagcgagggttcctctaccgagcgcgctgctgcggaga | 63 |
| DB | 50 gaagatttgtaaaccccgagcgaggtctcgtctaccgagcgcgctgctgcggaga | 109 |
| OY | 64 ccccgggtgtagcgcacgcgtcatcagtctgcagcaggagcaaaccttcaactgagac | 123 |
| DB | 110 cccccgggtgtagcgcacgcgtcatcagtctgcagcaggagcaaaccttcaactgagac | 169 |
| OY | 124 ttgggggataagaaacagatgatatataactaaactaaagtattggacagatagacgt | 183 |
| DB | 170 ttgggggataagaaagaggttgatatatatataactaaactaaagtattggacagatagacgt | 229 |
| OY | 184 gagattcaactcaaatgtaaatbaacaacacatctcaagaacctcaagaatcatactgt | 243 |
| DB | 230 gagattcaactcaaatgtaaatbaacaacacatctcaagaacctcaagaatcatactgt | 289 |
| OY | 244 caaagacaggggtgttccaatgaattcaactcaggtttctcttggagggtcagagaattgct | 303 |
| DB | 290 caaagacaggggtgttccaatgaattcaactcaggtttctcttggagggtcagagaattgct | 349 |
| OY | 304 gataatcatactccaaaagaactcgtggaatgagaaagaagatgtaattgaattatcacg | 363 |
| DB | 350 gataatcatactccaaaagaactcgtggaatgagaaagaagatgtaattgaattatcacg | 409 |
| OY | 364 gaacaaagcgggggtgatcattcaacagtttagatatctcttttatttttttcttcctc | 423 |
| DB | 410 gaacaaagcgggggtgatcattcaacagtttagatatctcttttatttttttcttcctc | 469 |
| OY | 424 aaatcctttttttaaaaaatagtccttttgtaatgvtgvtttcaaaaaggattgaa | 483 |
| DB | 470 aaatcctttttttaaaaaatagtccttttgtaatgvtgvtttcaaaaaggattgaa | 529 |
| OY | 484 aactgacaccccatctcttgaacaatcttgttaatttggaaattagtgctcatlcat | 543 |
| DB | 530 aactgacaccccatctcttgaacaatcttgttaatttggaaattagtgctcatlcat | 589 |

[illegible]

| | | |
|----|--------------|--------------|
| PR | 23-MAY-1997; | 97US-0047599 |
| PR | 23-MAY-1997; | 97US-0047600 |
| PR | 23-MAY-1997; | 97US-0047601 |
| PR | 23-MAY-1997; | 97US-0047613 |

23-MAY-1997; 97US-0047613

| | | |
|----|--------------|--------------|
| PR | 23-MAY-1997; | 97US-0047615 |
| PR | 23-MAY-1997; | 97US-0047617 |

| | | |
|----|--------------|--------------|
| PR | 23-MAY-1997: | 97US-0047632 |
| PR | 23-MAY-1997: | 97US-0047618 |

| | | |
|----|-------------|---------------|
| PR | 06-JUN-1997 | 9705-00483664 |
| PR | 06-JUN-1997 | 9705-00483974 |
| PR | 13-JUN-1997 | 9705-00496100 |
| PR | 08-JUL-1997 | 9705-00519266 |
| PR | 16-JUL-1997 | 9705-00528784 |
| PR | 18-AUG-1997 | 9705-00535724 |
| PR | 22-AUG-1997 | 9705-00556630 |
| PR | 22-AUG-1997 | 9705-00556631 |

22-AUG-1997; 97US-0056632

22-AUG-1997; 97US-0056637

22-AUG-1997; 97US-0056664

22-AUG-1997; 97US-0056862

22-AUG-1997; 97US-0056864
22-AUG-1997; 97US-0056873

22-AUG-1997; 97US-0056874.

22-AUG-1997; 97US-0056876.

22-AUG-1997; 97US-0056878

22-AUG-1997; 97US-0056879.

22-AUG-1997; 97US-0056881.

100

22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057659.
 PR 12-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.

(HUMA-) HUMAN GENOME SCI INC.

XX Bedmarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
 PI Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;

WPI: 1998-506364/43.
 P-PSDB; AAM74777.

XX New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders

PS Claim 1; Page 279-280; 721pp; English.

XX This sequence represents a nucleic acid molecule designated Gene 47 from
 CC the human CDNA clone HOGAV75 (deposited as clone ATCC 97899 and ATCC
 CC 209045) which encodes a secreted human protein. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAM74731-W5026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new
 CC polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).

XX Sequence 1220 BP; 382 A; 207 C; 258 G; 372 T; 1 other;

Query Match 61.1%; Score 895; DB 19; Length 1220;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1065; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 4 gaagattgttaaaccccgagcgaggttctgtcttaaccgagcgctgtctgcgagaga 63
 DB 44 gaagattgttaaaccccgagcgaggttctgtcttaaccgagcgctgtctgcgagaga 103
 QY 64 ccccggttgaagcaccgcatcatatgtctgacagagaggaacacctaactgaagagac 123
 DB 104 ccccggttgaagcaccgcatcatatgtctgacagagaggaacacctaactgaagagac 163
 QY 124 ttgggggataaagaagaagtgaaataataactcaagtcattgtgacagagatagcagt 183
 DB 164 ttgggggataaagaagaagtgaaataataactcaagtcattgtgacagagatagcagt 223
 QY 184 gagattcactcaaaagtgaataatgacacacatctccaagaagaactaaagaatctactgt 243
 DB 224 gagattcactcaaaagtgaataatgacacacatctccaagaagaactaaagaatctactgt 283

QY 244 caaagcagaggtgttccaatgaatctcaggttctctcttgaagggtcagaagatgct 303
 DB 284 caaagcagaggtgttccaatgaatctcaggttctctcttgaagggtcagaagatgct 343
 QY 304 gataataactccaagaagacttggaatgaggaagaagaatgtatgataagttatcag 363
 DB 344 gataataactccaagaagacttggaatgaggaagaagaatgtatgataagttatcag 403
 QY 364 gaacaacgggggttcatacacaagttagatlatctttatcttttttttttttttttt 423
 DB 404 gaacaacgggggttcatacacaagttagatlatctttatcttttttttttttttttt 463
 QY 424 aatccttt 483
 DB 464 aatccttt 523
 QY 484 aacgtgcacccatctcttgaacatctgttaattgaattcagtgtcatattatcat 543
 DB 524 aacgtgcacccatctcttgaacatctgttaattgaattcagtgtcatattatcat 583
 QY 544 tatgtttgttttcaatgtctgtattttgtgtatcaagctcagctcccttatattac 603
 DB 584 tatgtttgttttcaatgtctgtattttgtgtatcaagctcagctcccttatattac 643
 QY 604 cctctccttttaaaatctacgtgtgcacagagaggtacacttttcagacattgcat 663
 DB 644 cctctccttttaaaatctacgtgtgcacagagaggtacacttttcagacattgcat 703
 QY 664 ttcaagctgtgtgataataagaatgcacaatgcaagtggttcaataatgacttccaat 723
 DB 704 ttcaagctgtgtgataataagaatgcacaatgcaagtggttcaataatgacttccaat 763
 QY 724 tggccctgatgttc-actatgtgattacttctccttgactgacttcaatgtgagaga 782
 DB 764 tggccctgatgttc-actatgtgattacttctccttgactgacttcaatgtgagaga 823
 QY 783 tggaaattttcagaagaactgactgtgaaatgacattccttaacttgaagactact 842
 DB 824 tggaaattttcagaagaactgactgtgaaatgacattccttaacttgaagactact 883
 QY 843 tttaaaatttgaggtctgacccaagaagaagaaggaattcaggtgaggtcagaatgaca 902
 DB 884 tttaaaatttgaggtctgacccaagaagaagaaggaattcaggtgaggtcagaatgaca 943
 QY 903 gataaagttagagtaatgacttaactccaagaatggttcaactgaaagaagacatttaa 962
 DB 944 gataaagttagagtaatgacttaactccaagaatggttcaactgaaagaagacatttaa 1003
 QY 963 gatttttaaaaatctgttcagaagaatccagaagaaggttcaatttcaatgcaattaa 1022
 DB 1004 gatttttaaaaatctgttcagaagaatccagaagaaggttcaatttcaatgcaattaa 1063
 QY 1023 taaagctatacatgacagaatgatacaagaagacgtctctttt 1069
 DB 1064 taaagctatacatgacagaatgatacaagaagacgtctctttt 1110

RESULT 4

AAZ35859 standard; cDNA; 1514 BP.

AAZ35859; (first entry)

03-FEB-2000

Human sentrin nucleotide sequence.

Human; sentrin; antisense oligonucleotide; phosphorothioate;

Inhibition; modulation; expression; diagnosis; ss.

Homo sapiens.

Location/Qualifiers

Key

Best Local Similarity 99.7%; Pred. No. 1.2e-131;
Matches 350; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 gaagatttgaaccccgagagaggttctgtcttaccgagcgctgtgtcgagaga 63
 Db 43 gaagatttgaaccccgagagaggttctgtcttaccgagcgctgtgtcgagaga 102
 QY 64 ccccggttgaagcccgatcatatgtctgaccagaggaacacccaacttgaagac 123
 Db 103 ccccggttgaagcccgatcatatgtctgaccagaggaacacccaacttgaagac 162
 QY 124 ttgggggataagcaaggtgataatataaactcaaatgcatgtgacagagtaagcagt 183
 Db 163 ttgggggataagcaaggtgataatataaactcaaatgcatgtgacagagtaagcagt 222
 QY 184 gagattcattcaaaagttaaaaatgacacacatctcaagaacccaagaatcattgt 243
 Db 223 gagattcattcaaaagttaaaaatgacacacatctcaagaacccaagaatcattgt 282
 QY 244 caaagacaggggttccaatgtaattcactcaggttctcttggagggtcagagaattgtc 303
 Db 283 caaagacaggggttccaatgtaattcactcaggttctcttggagggtcagagaattgtc 342
 QY 304 gataatcattcacaagaactgggaatgaggaagaagatgtgattgaa 354
 Db 343 gataatcattcacaagaactgggaatgaggaagaagatgtgattgaa 393

RESULT 6
 AAT63339
 ID AAT63339 standard; cDNA; 372 BP.

XX AC AAT63339;

XX DT 17-AUG-1997 (first entry)

XX DE Human host cell protein NPI-6 partial cDNA clone.

XX KM Host cell protein; NPI-6; nucleoprotein interactor 6;

XX KW Influenza virus; replication; antiviral; virucide; ss.

XX OS Homo sapiens.

XX PN MOJ712967-A1.

XX PD 10-APR-1997.

XX PF 06-OCT-1995; 95MO-US13044.

XX PR 06-OCT-1995; 95MO-US13044.

XX PA (MOUN) MOUNT SINAI MEDICAL CENT.

XX PI Oneill R. Palese P;

XX DR WPI; 1997-226211/20.

XX PT New isolated DNA which encodes viral interacting proteins - used in
 assays to isolate products for inhibiting viral protein binding
 XX which is required for infection, replication, assembly or release

XX PS Disclosure; Fig 11; 98pp; English.

XX CC cDNA clones (AAT63335-39) comprise partial sequences for human
 CC nucleoprotein interactor proteins NPI-2 to NPI-6, respectively.
 CC These are host cell proteins which interact with influenza virus
 CC nucleoprotein (NP) and which may be accessory proteins required for
 CC influenza virus replication. NPI-6 was identified as a novel
 CC protein sequence. NPI sequences were isolated by interactive trap
 CC selection using LexA-NP as bait and yeast transformed with an HeLa
 CC cDNA library. NPI-1 (see also AAT63334) and NPI-2 to NPI-6 cDNAs were
 CC cloned and analysed. The clones can be used to produce human NPI
 CC proteins for use in identifying cpds. that inhibit viral

CC replication.

XX SQ Sequence 372 BP; 121 A; 72 C; 97 G; 82 T; 0 other;

Query Match 19.4%; Score 284; DB 18; Length 372;
 Best Local Similarity 99.7%; Pred. No. 4.2e-124;
 Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 atttgaaccccgagagaggttctgtcttaccgagcgctgtgtcgagagacccc 68
 Db 1 atttgaaccccgagagaggttctgtcttaccgagcgctgtgtcgagagacccc 60
 QY 69 gggtaagccacccgcatcatatgtctgaccagaggaacacccaacttgaagacttgag 128
 Db 61 gggtaagccacccgcatcatatgtctgaccagaggaacacccaacttgaagacttgag 120
 QY 129 gataagaagcaaggtgataatataaactcaaatgcatgtgacagagtagcagtgagat 188
 Db 121 gataagaagcaaggtgataatataaactcaaatgcatgtgacagagtagcagtgagat 180
 QY 189 tcacttcaaaagtgaatgaacacacatctcaagaactcaagaatcacaactgtgcaag 248
 Db 181 tcacttcaaaagtgaatgaacacacatctcaagaactcaagaatcacaactgtgcaag 240
 QY 249 acaaggtgttccaatgtaattcactcaggttctcttggagggtcagagaattgtgtaa 308
 Db 241 acaaggtgttccaatgtaattcactcaggttctcttggagggtcagagaattgtgtaa 300
 QY 309 tcacttcaaaagaacttgggaatgaggaagaag 343
 Db 301 tcacttcaaaagaacttgggaatgaggaagaag 335

RESULT 7

AAF59399
 ID AAF59399 standard; DNA; 372 BP.

XX AC AAF59399;

XX DT 02-MAY-2001 (first entry)

XX DE Human host cell protein NPI-6 partial nucleotide sequence SRQ ID NO:11.

XX KM Identification; antiviral; viral protein; viral replication; NP;

XX KW viral infection; nucleoprotein; ds.

XX OS Homo sapiens.

XX OS WO200111335-A2.

XX PD 15-FEB-2001.

XX PF 11-AUG-2000; 2000MO-US22257.

XX PR 11-AUG-1999; 9905-0148263.

XX PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.

XX PI O'Neill R. Harty R. Palese PM;

XX DR WPI; 2001-168816/17.

XX PT Identifying a substance that inhibits the interaction between a viral
 protein and a host cell protein, useful for the discovery of new
 XX antiviral compounds -

XX PS Disclosure; Fig 11; 147pp; English.

XX CC The present invention describes a method (M1) for identifying a
 CC substance that inhibits the interaction of a viral protein (VP) with a
 CC host cell protein (HP). The method comprises: (a) contacting HP with VP
 CC in the presence of a test substance; and (b) detecting complex formation,

CC where the ability of the test substance to inhibit HP/VP interaction is
 CC indicated by a decrease in complex formation. The antiviral compounds
 CC that inhibit the interaction between a host protein (NSI-IP or NPI-1)
 CC and a viral protein (NSI) are useful for treating or inhibiting viral
 CC infection, preferably influenza and rhinovirus infection, in humans.
 CC Antiviral compounds include peptides and antibodies. In particular,
 CC compositions comprising a polypeptide containing an amino acid sequence
 CC corresponding to the NP-MS domain of the influenza virus NP protein,
 CC which inhibits the specific interaction of the NPI-1 protein with the
 CC influenza virus NP protein are useful for treating or inhibiting
 CC influenza viral infection in humans. The present sequence represents a
 CC human host cell protein NPI-6 partial nucleotide sequence, which is used
 CC in the exemplification of the present invention.
 CC
 CC Sequence 372 BP; 121 A; 72 C; 97 G; 82 T; 0 other;

Query Match 19.4%; Score 284; DB 22; Length 372;
 Best Local Similarity 99.7%; Pred. No. 4.2e-124;

Matches 334; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 attgtgaaccccgagcgaggttctgtaccggagccgctgtgtcgagagacc 68
 Db 1 attgtgaaccccgagcgaggttctgtaccggagccgctgtgtcgagagacc 60
 QY 69 ggggtgaagccacccgtcatctgtgtaccagagagcaaaccttcaactgagacttgg 128
 Db 61 ggggtgaagccacccgtcatctgtgtaccagagagcaaaccttcaactgagacttgg 120
 QY 129 ggtatgaagcagcaggtgatataataaactcaagtcattgtgacagagatgagat 188
 Db 121 ggtatgaagcagcaggtgatataataaactcaagtcattgtgacagagatgagat 180
 QY 189 tcaactcaagtgaaatgacacacacatctcaagaactcaagaatcatatgtcaag 248
 Db 181 tcaactcaagtgaaatgacacacacatctcaagaactcaagaatcatatgtcaag 240
 QY 249 acaaggtgttccaatgaattcactcaggtttctcttgaaggtcagagaattgtgtatga 308
 Db 241 acaaggtgttccaatgaattcactcaggtttctcttgaaggtcagagaattgtgtatga 300
 QY 309 tcaactccaagaagactggtgaatgagagaag 343
 Db 301 tcaactccaagaagactggtgaatgagagaag 335

RESULT 8

AAT03735
 ID AAT03735 standard; cDNA; 425 BP.

AC AAT03735;

DT 26-MAR-1996 (first entry)

DE TNF-R p55IC/Fas-IC-binding protein DD11 cDNA clone.

KW Tumour necrosis factor receptor; TNF-R; p55IC; Fas-IC;
 intracellular domain binding protein; ss.

KM Homo sapiens.

OS Homo sapiens.

PN W09531544-A1.

PD 23-NOV-1995.

PF 11-MAY-1995; 95MO-US05854.

PR 02-OCT-1994; 94IL-0111125.

PA 11-MAY-1994; 94IL-0109632.
 (WEIN/) WEINMURZEL H.
 (YEDA) YEDA RES & DEV CO LTD.

PI Boldin M, Melt I, Varfolomeev E, Wallach D;
 DR WPI; 1996-010930/01.
 XX
 PT TNF-NGF receptor superfamily intracellular domain-binding proteins -
 PT useful for modulating receptor function, e.g. for treating tumours
 PT or HIV-infected cells
 PS Claim 18; Fig 12; 96pp; English.
 CC CDNA clone DD11 (AAT03735) was isolated by screening a human HeLa
 CC library using the human tumour necrosis factor receptor (TNF-R)
 CC p55 death domain (p55D) as 'bait'. The full length of the DD11
 CC transcript is approx 1.2 kb. The protein encoded by cDNA DD11
 CC interacts strongly with p55D (amino acids 326-414) and also with
 CC human and mouse FAS intracellular domain. Such proteins may
 CC be used modulate TNF-R function.
 CC
 CC Sequence 425 BP; 135 A; 80 C; 115 G; 95 T; 0 other;

Query Match 13.4%; Score 197; DB 17; Length 425;
 Best Local Similarity 100.0%; Pred. No. 4.1e-83;

Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 140 aaggtgaatataataaactcaagtcattgtgacagagatgagatgagatcactcaag 199
 Db 171 aaggtgaatataataaactcaagtcattgtgacagagatgagatgagatcactcaag 230
 QY 200 tgaatgacacacacatctcaagaactcaagaatcatatcttcaagaaggtgttc 259
 Db 231 tgaatgacacacacatctcaagaactcaagaatcatatcttcaagaaggtgttc 290
 QY 260 caatgaattcactcaggtttctcttgaaggtcagagaattgtgataatcactca 319
 Db 291 caatgaattcactcaggtttctcttgaaggtcagagaattgtgataatcactca 350
 QY 320 aagaactgggaatggag 336
 Db 351 aagaactgggaatggag 367

RESULT 9

AAT19668
 ID AAT19668 standard; cDNA to mRNA; 180 BP.

AC AAT19668;

DT 28-JUN-1996 (first entry)

DE Human gene signature HDWG00738.

KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;
 human; cloning; mapping; non-biased library; diagnosis; detection;
 cell typing; abnormal cell function; ss.

OS Homo sapiens.

PN W09514772-A1.

PD 01-JUN-1995.

PF 11-NOV-1994; 94MO-JP01916.

PR 12-NOV-1993; 93JP-0355504.

PA (MATS/) MATSUBARA K.
 (OKUBO/) OKUBO K.

PI Matsubara K, Okubo K;

DR WPI; 1995-206931/27.

PT Identifying gene signatures in 3'-directed human cDNA library - e.g.
 PT for diagnosis of abnormal cell function, by preparing cDNA that
 PT reflects relative abundance of corresp. mRNA in specific human
 PT tissues

XX
 PS Claim 1; Page 445; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
 CC given in AAT19001-T26837 and which is able to hybridise to part of
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
 CC sequences were obtained from 3'-directed cDNA libraries prepared
 CC from various human tissues; synthesis of cDNA was initiated from the
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
 CC untranslated sequence is unique to a particular mRNA species, almost
 CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
 CC is constructed so as to reflect accurately the relative abundance of
 CC different mRNAs in the particular tissue from which it was derived.
 CC The appearance frequency of a given GS in a cDNA library can be
 CC determined (esp. using primers and probes derived from the GS
 CC sequences) as a means of diagnosing abnormal cell function or for
 CC recognising different cell types.

XX
 SQ Sequence 180 BP; 65 A; 26 C; 26 G; 63 T; 0 other;

Query Match 5.8%; Score 85; DB 16; Length 180;

Best Local Similarity 100.0%; Pred. No. 2.4e-30;

Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1071 gatttattgtactcttggcctggtgatatgggtttaaatgacattgctgtaccag 1130

|||||

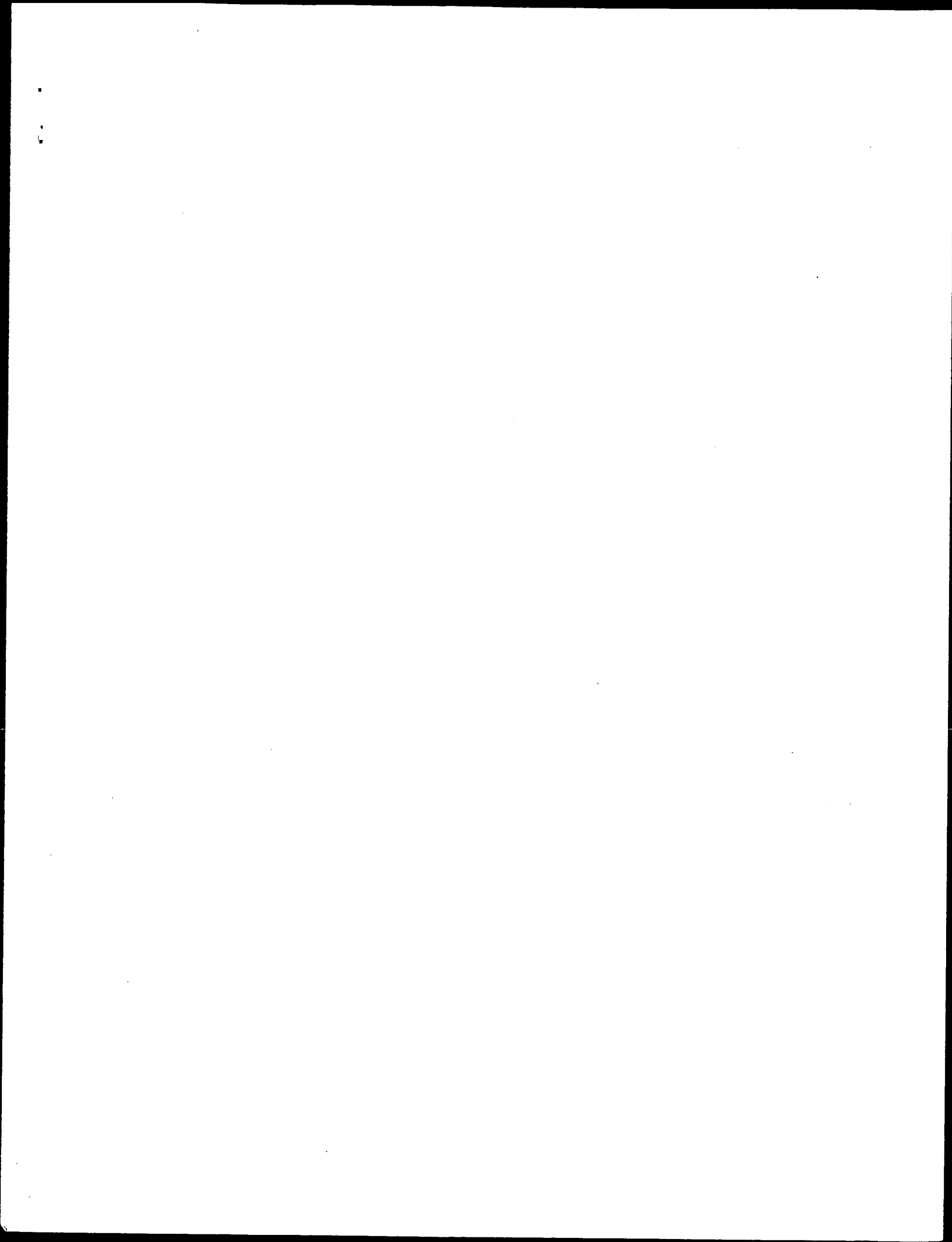
DB 84 gatttattgtactcttggcctggtgatatgggtttaaatgacattgctgtaccag 143

OY 1131 cttcataaataacaataatttgt 1155

|||||

DB 144 cttcataaataacaataatttgt 168

Search completed: August 17, 2001, 11:22:29
 Job time: 4394 sec



GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2001, 09:30:24 ; Search time 1171.13 Seconds
(without alignments)
11824.845 Million cell updates/sec

Title: us-09-484-964-1

Perfect score: 1465
Sequence: 1 cgggaagattgtaaaccc.....gataaatggcattgccagcc 1465

Scoring table: OLIGO_NUC
Gapop 60.0 , Capext 60.0

Searched: 10228115 segs, 4726426750 residues

Word size : 50

Total number of hits satisfying chosen parameters: 566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

BST:*

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1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. .1046

| Query Match | Best Local Similarity | Matches | 911; Conservative | 47.2%; Score 691; DB 106; Length 1046; | 99.7%; Pred. No. 0; | 0; Mismatches | 2; Indels | 1; Gaps | 1; |
|-------------|--|---------|-------------------|--|---------------------|---------------|-----------|---------|----|
| QY 4 | gaagagttgttaaaccccgagacgagaggttcctgcttaccgagagccgctgctgtgcygagaa | 63 | | | | | | | |
| Db 35 | GAAGGATTTGTAAACCCCGAGCGAGGTTGCTTACCAGGCGCTGCTGTGCGGAGA | 94 | | | | | | | |
| QY 64 | cccccggtgaagccaccgtcactcgtctgtaccagagagcaaaacctcaactgagagc | 123 | | | | | | | |
| Db 95 | CCCCCGGTGAAGCCCGCTCATGTCTGACCAAGGAGCGAAMACCTTCAACTGAGGAC | 154 | | | | | | | |
| QY 124 | ttaggggataaagaagaagtgaatatatttaacctcaagtcattgagacagatagcagt | 183 | | | | | | | |
| Db 155 | TTGGGGGATTAAGAGGAAGTGTAATTAATTAACCTCAAGACATTTGACGAGATACAGT | 214 | | | | | | | |
| QY 184 | gaattcacttcaaaagtgaatatgtgacaacatctcaagaacctcaagaatcaactagt | 243 | | | | | | | |
| Db 215 | TNATTCACCTTCAAGGTGAATATGACACACATCTCAAGAACTCAAGAAATATATCTGT | 274 | | | | | | | |
| QY 244 | caaaagcaagtggttccaatgaatctactcaggttctctttagaggttcagagaattgct | 303 | | | | | | | |
| Db 275 | CAAAAGCAGAGGTTTCCATGATCAATCACTCAGGTTTCTTTTGAGGCTGAGAAATTCCT | 334 | | | | | | | |
| QY 304 | ataatacatcattccaaagaagaattgaaatgaaagaaataaataatgatttaactttatcga | 363 | | | | | | | |

Db 395 GAACAAACGGGGGTCATCAACAGTTAGATCTTTTATTTTCTTTCCAC 454
 |||
 Qy 424 aatcccttttlaatttlaaataatgcttccttgaatgctgcttcaaacggaattga 483
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 Db 455 AATCCCTTTTATTTTAAAAATAGTCTTTTGTAAAGTGCTGTCAANCGAATTGA 514
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 Qy 484 aactgaccccatctcttgaacatctgtaattgaattcagtgctcaattatcat 543
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 Db 515 AACTGGACCCCATCTCTTTGAAACATCGTATTTGAATCTAGTGCATATTATCAT 574

Db 575 TATTGTTGTTTTCATGTGCTGATTTTGGTGATCAAGCCTCAGTCCCTCATATTAC 634
|||||
OY 604 ccctcctctttaaaattacgtgtgcacagagaggtccactcttcaggacattgcat 663
|||||
Db 635 CCTTCCTTTTTTAAAAATTTACGTGTGACAGAGAGGCTACCTTTTTTCAGGACATTTGCATT 694
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OY 664 ttcaagcttggtgtaataaagatcgaccatgcaaggtgttcaataatgacttccaat 723
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 Db 695 TTCAGGCTTGTGGTGAATTAAGATCGACCAATGCAAGTGTTCATATGACTTTCCAAAT 754
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 OY 724 tggccctgtagtgc-agcagtgtacttacttactccttgagctgtgacttcaagtggaga 782
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 Db 755 TGGCCCTGATGTTCTAGCATGATTACTTCACTCCCTGAGCTGACTGCTTCACTGAGGAGA 814
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 OY 783 tggaaatttttgcagaagactgagctgtgaaaatgaccccttcccttacttgaagctact 842
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 Db 815 TGGAAAGTTTTCAGAGACTGAACTGTGAAAAATGACCTTCTTACTTGAAGCTACT 874
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 OY 843 tttaaaatttgaggtctgagccaaaagaagagatatacaggttgaagtcagaatgaca 902
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 Db 875 TTTAAATTTGAGGCTGTGAGCAAAAGAGAGATATCAGTTGAAGTCAAGATGACA 934
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 OY 903 gataagctgagagt 916
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RESULT 2
 AL544942 898 bp mRNA EST 16-FEB-2001
 LOCUS AL544942 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0D1012YA10 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL544942
 VERSION AL544942.1 GI:12877423
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 898)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope - Centre National de Sequencage
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1. 898

FEATURES
 source
 1. 898
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0D1012YA10"
 /clone_lib="LTI_NFL006_PL2"
 /issue_type="placenta"
 /note="Vector: PCWSPORT 6; Site_1: NotI; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the PCWSPORT 6
 vector. Library was normalized. Library was constructed by
 Life Technologies. Contact : Feng Liang Life Technologies,
 a division of Invitrogen 9800 Medical Center Drive
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
 Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com"

BASE COUNT 259 a 160 c 200 g 275 t 4 others
 ORIGIN

Query Match 46.6% Score 683 DB 106 Length 898
 Best Local Similarity 99.9% Pred. No. 0
 Matches 733 Conservative 0 Mismatches 1 Indels 0 Gaps 0

OY 4 gaagattgttaaaccccgagagaggtctgtcttaccgagcgctgtctgagaga 63
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 Db 11 GAAGATTGTGAAACCCCGAGAGAGGTCTGTCTTACCAGCGCGCTGCTGGGAGA 70
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 OY 64 ccccggtgagccacgcgtatcatgtctgacagagagcaaaccttaactgagagc 123
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Db 71 CCCCCGGGTGAAGCCACCGTCATCATGTGACCAAGGACGCAAAACCTTCACTGAGGAC 130
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 OY 124 ttgggagataagaagcaaggtgatatataatcaaaagctatggacagagtagcagt 183
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 Db 131 TTGGGGGATTAAGAAGAGAGGTGATATATTAACCTCAAACTCATTTGACAGATAGCAGT 190
 |||||||
 OY 184 gagattcacttcaaatgtgaaatgacacacatctcaagaactcaagaatatactgt 243
 |||||||
 Db 191 GAGATTCATCTCAAAAGGAAATGACACACATCTCAAGAAACTCAAGAAATCATCTGT 250
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 OY 244 caaagacaggtgttccatgaaatcactcaggttctcttcttgaaggtcagaaatgtc 303
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 Db 251 CAAGACAGAGGTGTTCATGAATGATTCACAGTTCCTCTTGAAGGCTCAGAGATAGCT 310
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 OY 304 gataatcactcccaaaagaactgaggaatgagagaaagatgtgatgttcaatcag 363
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 Db 311 GATTAATCATCTCCAAAAGAACTGGGAATGAGGACAAAGATGATGAAATGATTCAG 370
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 OY 364 gaacaaacgggggtgcatcaacagttatgatatctcttcttcttcttccctc 423
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 Db 371 GAACAAACGGGGGTCAATTCACAGTTAGATATCTTTTATTTTCTTTCCCTC 430
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 OY 424 aatccttttattttaaataatagttcttcttgaatgtgtgttcaaaacgaaattgaa 483
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 Db 431 AATCCTTTTATTTTAAAAATAGTTCTTTTGAATGTGTTCAAAACGGAATTGAA 490
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 OY 484 aactggaacccatctcttgaacacatctgtaatttgaaattcaggtccattatcat 543
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 Db 491 AACGGCAACCCCATCTTTGAAACATCGTAATTTGAATTCAGTGCATATTCAT 550
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 OY 544 tatgtttgtttcatgtctgagtttcttcttcttcttcttcttcttcttcttcttctt 603
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 Db 551 TATGTTTGTGTTTATGTTGCTGATTTTGTGATCAAGCTCAGTCCCTCATATTTAC 610
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 OY 604 cctctcctttaaataatlacgtgtgcacagagaggtccacttcaagaacatgtcatc 663
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 OY 664 ttcaagcttggtgtaataaagatcgaccatgcaaggtgttcaataatgacttccaat 723
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 Db 671 TTCAGGCTTGTGGTGAATTAAGATCGACCAATGCAAGTGTTCATATGACTTTCCAAAT 730
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 OY 724 tggccctgtagtgc 737
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 Db 731 TGGCCCTGATGTTC 744
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RESULT 3
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 LOCUS AL533666 LTI_FL013_FBrn1 Homo sapiens cDNA clone CS0DF002Y003 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL533666
 VERSION AL533666.1 GI:12797159
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 907)
 Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope - Centre National de Sequencage
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers

FEATURES

source
 1. 907
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DF002Y003"
 /clone_lib="LTI_FL013_FBrn1"

/dev stage="pooled tissue from post conception fetuses (20 week, 24 week and 26 week)"
 /lab host="DH10B"
 /note="Organ: Fetal brain; Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 253 a 166 c 206 g 280 t 2 others

ORIGIN

Query Match 46.6%; Score 683; DB 106; Length 907;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 733; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 364 gaacaaagggggggtcattcaacagtttagatattcttttctttctctc 423
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RESULT 4
 AL583458 913 bp mRNA EST 16-FEB-2001
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 DEFINITION
 AL583458 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0DL012YD05 5 prime, mRNA sequence.
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 AL583458
 VERSION
 AL583458.1 GI:12952440
 KEYWORDS
 EST.
 SOURCE
 human.
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE
 1 (bases 1 to 913)
 Li, W.-B., Gruber, C., Jessee, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 Bp 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Qualifiers
 1. 913
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_id="CS0DL012YD05"
 /clone_1lb="LTI_NFL010_BC2"
 /sex="male"
 /tissue_type="B cells from Burkitt lymphoma"
 /note="Vector: PCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the PCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

FEATURES

source

BASE COUNT 268 a 166 c 199 g 279 t 1 others

ORIGIN

Query Match 46.3%; Score 679; DB 106; Length 913;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 849; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 75 agccacgctcatctgctcagcagaggaacaaacctcaactgaggaactggggataa 134
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 61 AGCCACCGTCAATCTGCTGACCGAGGCAAAACCTTCAACTGAGCACTTGGGGGATTA 120
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 135 gaacgaagtgaaataataaactcaagatcattgagcagatagacgtagattcaact 194
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 121 GAAGGAAGGTGAATATTTAACTCAAGATGATGACAGGATGAGATGATCACTT 180
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 195 caaagtgaatgacaacacatctcaagaactcaagaactcaactgataagaagaagg 254
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 181 CAAGTGAATATGACACATCTCAAGAAATCAAGAAATCAATGATGATGATGATGATGAT 240
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 255 tgttcaatgaaatcactcaggtctctcttggaggtcagaagaatgctgataatacat 314
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 241 TGTTCATGAAATCACTGCAAGGTTCTCTTTGAGGGTCAAGAAATGCTGATATATCATAC 300
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 315 tccaaagaactgggaatggaggaagaagtgtgattgaagttatcagaacaaacagg 374
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 301 TCAGAAAGAACTGGGAATGAGAGAGAGAGATGTGATTTATTCAGGAACAAACGGG 360
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 375 gggtcattcaacagtttagatatcttttatttttttcttctcctcaatccttttt 434
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Db 361 GGGTCATTCACAGCTTAGATATCTTTTATTTTCTTTTCCCTCAATCCTTTT 420
 QY 435 atttcaaaatagctcttctgtatgtgtgttcaaaacggaattgaacatgaccc 494
 Db 421 ATTTTAAATATATCTTTTGTATGTGTTCAAAGGAATGAAATGACGACCC 480
 QY 495 catctcttgaacatcgtglaattgaattcagtcctcattatcattgtgtt 554
 Db 481 CATCTCTTGAACATCGTGAATTTGAATTCAGTGTCTATTTATTTATTTGTT 540
 QY 555 ttcatgttcgatttttgggtatcaagccctcagtcctcattatcattcctt 614
 Db 541 TTCAATGTGCTGATTTTGGTATCAAGCTTCCCTTCAATTTACCTCTCTCTT 600
 QY 615 taaataatcgtgtgcaagaagagtcaccttctcaggaacatgacattcagctgt 674
 Db 601 TAAATAATACGTGTGACAGAGAGTGTACCTTTTTCAGACATTCGATTTTCAGCTTGT 660
 QY 675 ggtgataataatgacgaacgaagtgatcattcattatgacattcgaattg 734
 Db 661 GGTGATTAATTAAGATCGCAATGCAATGTTCAATTAAGCTTTCCAAATTTGCCCTGATG 720
 QY 735 ttc-agcatgtatctactcactcctgactgactgactcagtgagatggaattt 793
 Db 721 TTTCAGCATGTGATTTACTTCACTCTGACATGTGACTTTTCAGTGGAGATGGAATTTT 780
 QY 794 cagaagaactgactgtggaataatgacattcctcactaactgaagctactttaaat 853
 Db 781 CAGGAACACTGAACGTGGAATAATGACCTTCTTAACTGAAGCTATTTAAATTTG 840
 QY 854 aggtctggac 864
 Db 841 AGGCTGTGGAC 851

RESULT 5
 AL521484 868 bp mRNA EST 13-FEB-2001
 LOCUS AL521484 LTI_NFL004_NBC2 Homo sapiens CDNA CS0DB001YN17 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL521484
 VERSION AL521484.1 GI:12784977
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 868)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
 Location/Dnaifiers
 1. .868
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DB001YN17"
 /clone_id="LTI_NFL004_NBC2"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain. Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(OT) primer. Five prime end
 enriched, double-stranded cDNA was digested with Not I and
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6
 vector. Library was normalized. Library was constructed
 by life technologies. Contact : Feng Liang life
 Technologies, a division of invitrogen 9800 Medical Center
 Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
 8371 Email : fliang@lifetech.com URL :

BASE COUNT 261 a 151 c 186 g 270 t
 ORIGIN
 Query Match 44.0% Score 645; DB 105; Length 868;
 Best Local Similarity 99.7%; Pred. No. 0;
 Matches 865; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 56 tgcgaagaccccggttaagcaccgctcatcagtcctcagcaggaagcacaacttcaa 115
 Db 1 TGGCGAGACCCCGGGGTGAAGCAACCGTCATCATCTGTGACAGAGCAAAACCTTCAA 60
 QY 116 ctgaggaacttgggggataaagaacgaagtgaatatataactcaagtcattggacag 175
 Db 61 CTGAGGACTTTGGGGATTAAGAAGAGGTGAATATTAATCAAACTCAATGTGACAGG 120
 QY 176 atagagtgagattcactccaagtgaataatgacacacatcctcaagaactcaagaat 235
 Db 121 ATAGCGGTGAATTCATTTCAAGTGAATGACACACATCTCAAGAACTCAAGAAAT 180
 QY 236 catactgcaagaacgaagtglttccaatgaaattcactcaggtttcctcttgaagtcaga 295
 Db 181 CATACTGCAAAGACAGGGGTGTTCCATGAATTCACCTCAGGTTTCTTTGAGGGTCAGA 240
 QY 296 gaattgctgataataataataaagaactcgaagtgaggaagaagaatgattgag 355
 Db 241 GAATTTGCTGAATTAATCACTCCAAAAGACTGGGAATGAGGAAGAAAGATGATTTGAG 300
 QY 356 ttatcaagaacaaacgggggtcactcaacagtttaatalctcttatttcttct 415
 Db 301 TTTATCAGGAACAAACGGGGGTCAATTCACAGCTTAATATTTATTTATTTTCT 360
 QY 416 ttccctcaatccttcttattttaaataagtccttcttgaatgtgtgttcaaacg 475
 Db 361 TTTCCTCAATCTTTTATTTTAAAAATAGTTCTTTGTAATGTGTGTCAAAACG 420
 QY 476 gaattgaacactgcaacccatctcttgaacacatcgttaatttgaattcagtcga 535
 Db 421 GAATTTAAATACGGCACCCCATCTTTGAAACATCTGTGTAATTTGAAATTTAGTCTCA 480
 QY 536 ttatcattatgttcttcttcaatgtgtcatttgggtatcgaagcctcagtcctt 595
 Db 481 TTATTCATTAATGTTGTTTTCATGTCGTGATTTTGTGATCAAGCTCAGTCCCTT 540
 QY 596 catattaccctcctctttaaataatcagtgtagcagagaggtcaccttttgaagac 655
 Db 541 CATATTACCTCTCTCTTTTAAAAATTAAGTGTGACAGAGAGGTCACTTTTTCAGGAC 600
 QY 656 attgaattcagagcttgtgtgataaataagatcagacaaatgcaagtgltcataatgac 715
 Db 601 ATTGCATTTTTCAGGCTTTGTGTAATAATTAAGATGACCAATGCAAGTTCATTAATGAC 660
 QY 716 ttccaattggccctgatgttc-agcagtgaattactcactcctcgtgactgtacttca 774
 Db 661 TTTCCAATTTGGCCCTGAGTGTCTACATGATTAATCTTCACTCCGAGCTGTGATTTTCA 720
 QY 775 gtggagagatggaagtttttcaagaagaactggaactgtggaataatgaccttcaactg 834
 Db 721 GTGGAGATGGAAGTTTTCAGAGACTGAACGTGTGAAAAATGACTTTCCTTAACCTG 780
 QY 835 aagctactttaaataattgaggtctggaacaaagaagaagatatcaagttgaagtc 894
 Db 781 AAGCTACTTTTAAATTTGAGGGTGTGACCAAAAGAGAGGAATATCAGTTGAATGCA 840
 QY 895 agatgacagataagtgagagatgac 922
 Db 841 AGATGACAGATAAGGTGAGAGTAATGAC 868

RESULT 6
 BG541610 835 bp mRNA EST 03-APR-2001
 LOCUS BG541610

DEFINITION 602571169P1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695641 5', mRNA sequence.

ACCESSION BG541610

VERSION BG541610.1 GI:13533843

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 835)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabs-remail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:

<http://image.lnl.gov>

Plate: LNCM1521 row: 1 column: 18

High quality sequence stop: 792.

Location/Qualifiers

1. 835

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:4695641"

/clone_1id="NIH_MGC_77"

/lab_host="DH10B (T1 phage-resistant)"

/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site: 1; SfiI (ggccgctggcgc); Site: 2: SfiI (ggccattatggc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGACC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH-MGC Library."

BASE COUNT 232 a 154 c 192 g 257 t

ORIGIN

Query Match 41.6%; Score 610; DB 155; Length 835;

Best Local Similarity 99.8%; Pred. No. 4.1e-288;

Matches 660; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 gaagatttgaaccccgagaggttctgtctaccgagcgctgtgtcgaga 63

DB 25 GAAGATTGTGAACCCCGAGCGAGGTTCTGTCTTACCGAGCGCTGTGCGAGA 84

OY 64 ccccgagtggaagccacgcatcatgtctgacagagagcaaacctcaactgagac 123

DB 85 CCCCCGGGTGAAGCCACGTCATGTCGACGAGGCAAAACCTCACTGAGAGAC 144

OY 124 ttgggggataagagcaagtgatataataactcaagtcattgacagagatagcagt 183

DB 145 TTGGGGGATTAAGAGGAGGATATATATTAACCTCAAGTCATTGAGACAGATAGCAGT 204

OY 184 gagatcactcaagaatgaatgacacacatctcaagaaaccaaagaatctactgt 243

DB 205 GAGATTCCTTCAAGTGAATGACACACATCTCAAGAACTCAAGAACTTACTGCT 264

OY 244 caaagacagaggtgttccaatgaatcaactcaggttctcttggagggtcagaatgtct 303

DB 265 CAAAGACAGGGGTTCGAATGATTCAGTTCGTTTCTTGAAGGGTCAGAGATTGCT 324

OY 304 gataatcactcaaaagaacttgggaatggagagaagatgtgatgtgaattatcag 363

DB 325 GATAATCTACTCCAAAAGAACTGGGAATGAGAGAGAAAGTGTGATTAAGTTATCAG 384

OY 364 gaacaaacgggggtcattcaacaggttagatacttcttatttttttcttccctc 423

DB 385 GAACAAACGGGGGTCTATTCACAGCTTAGATTTCTTTTATTTTCTTTCCCTC 444

OY 424 aatcccttttattttaaanaatagttcttcttgaatgtgtgttcaaaacggaattgaa 483

DB 445 AATCCCTTTTATTTTAAANAATAGTTCTTTTGAATGTGTGTCAAAACGAATGAA 504

OY 484 aactgacacccatctcttgaacacatctgtgaatattgattctatgtctatctat 543

DB 505 AACTGGACCCCATCTCTTGAACATCTGGTAATTTGAATTTCTAGTGTCAATTATCAT 564

OY 544 tatgtttgtttcattgtgctgatttgggtgatacagcctcagtcctcattatc 603

DB 565 TATTTGTTTGTTCATTTGCTGATTTTGGTATTCAGCCTTCAGCTCATATTCAC 624

OY 604 cctctcctttaaanaatcagtgltgacagagaggttcaccttttcaaggaattgatt 663

DB 625 CCTCTCCTTTTAAANAATAGTGTGACAGAGAGCTACCTTTTCAGACATTCGATT 684

OY 664 t 664

DB 685 t 685

RESULT 7

AL532394 756 bp mRNA EST 13-FEB-2001

LOCUS AL532394 L7L_NFL001_NBC4 Homo sapiens cDNA clone CSODM014YH24 5

DEFINITION prime, mRNA sequence.

ACCESSION AL532394

VERSION AL532394.1 GI:12795887

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 756)

Li, W.B., Gruber, C., Jesse, J., and Polayes, D.

Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

CONTACT: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr.

Location/Qualifiers

1. 756

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSODM014YH24"

/clone_1id="L7L_NFL001_NBC4"

/sex="male"

/tissue_type="neuroblastoma cells"

/lab_host="DH10B"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: liang@life.com URL: <http://fulllength.invitrogen.com>"

BASE COUNT 218 a 140 c 161 g 236 t

ORIGIN

Query Match 40.4%; Score 592; DB 106; Length 756;

Best Local Similarity 100.0%; Pred. No. 2.7e-279;

Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 aataataactcaaacgattgacagagatagcagtgatgattcactcaagaatgaa 205

| Db | 149 | AATATATTAACCTCAAGGTCATTGGACGATGATGACGATGAGATTCACCTCAAAAGTGAAA | 208 |
|------------|--|---|-----|
| Oy | 206 | tgaacaacatctcaagaactcaagaatcaatcaatcctgtcaagaacaggggtgttccaatga | 265 |
| Db | 209 | TGACAAACCAATCTCAAGAACTCAAGAGATATCATCTGCAAAAGACAGGTTCTTCAATGA | 268 |
| Oy | 266 | atcaactcaggtttctctctttagaggtcagagaattgctgataatcatcactccaagaagac | 325 |
| Db | 269 | ATTCACTCAGGTTCTCTCTTGAAGGTCAGAAATTCGCTGATATCATATCTCCAAAAGAC | 328 |
| Oy | 326 | tgggaatggaagaagaatgtagtltgaagttacaggaacaacaggggggtcatcaca | 385 |
| Db | 329 | TGGCAATGAGAGAAAGATGTGATTGAACTTATTCAGGAACAACGGGGGTCATTCAA | 388 |
| Oy | 386 | cagtttagatatctcttatt | 445 |
| Db | 389 | CAGTTTAAATATCTCTTTTATTTTATTTTCTTTCCCTCAATCTTTTATTTTAAAAA | 448 |
| Oy | 446 | tagtctcttctgtaatgltgtgtlctaaacaggaatltgaaacatgagacccactcttga | 505 |
| Db | 449 | TAGTCTTTTGAATGTGTGTGTCAAAAACGGAATTTGAAAATGCGACACCCATCTCTTGA | 508 |
| Oy | 506 | aacatctgtaatttgaattcttagtgcataatcatcattatgtttgtttcattgtgc | 565 |
| Db | 509 | AACATCTGTGTAAATTTGAATTTCTATGCTCATTTATTCATTTATTTGTTTCATTGTGCT | 568 |
| Oy | 566 | gattttgtatacaagctcagtcacctatattacccctcctctctttttaaataacg | 625 |
| Db | 569 | GATTTTGTGATTCAGGCTCAGTCCCTTCATATTTACCTCTCTTTTAAATATACG | 628 |
| Oy | 626 | tgtcacagagaaggtcaccttttccaagaatctgcatlccaggtgtgtgtataata | 685 |
| Db | 629 | TGTGCAGAGAGGTCACCTTTTTCAGACATTCGATTTTCAGGCTGTGTGATAATA | 688 |
| Oy | 686 | agatgaccaatgcaagtggtcataatgaacttccaattggccctgtatgtc | 737 |
| Db | 689 | AGATCGACCAATGCAAGTGTTCATATATGATCTTTCCAAITGGCCCTGATGTTC | 740 |
| RESULT | 8 | | |
| LOCUS | BE888192 | | |
| DEFINITION | 601511710P1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3912914 5', | | |
| ACCESSION | BE888192 | | |
| VERSION | BE888192.1 | | |
| KEYWORDS | EST. | | |
| SOURCE | human. | | |
| ORGANISM | Homo sapiens | | |
| REFERENCE | Eukaryote; Metazoa; Chordata; Vertebrata; Euteleostomi | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | |
| TITLE | 1 (bases 1 to 858) | | |
| JOURNAL | NIH-MGC http://mgc.nci.nih.gov/ | | |
| COMMENT | National Institutes of Health, Mammalian Gene Collection (MGC) | | |
| | Unpublished (1999) | | |
| | Contact: Robert Strausberg, Ph.D. | | |
| | Email: rgs@bhs-remail.nih.gov | | |
| | Tissue Procurement: ATCC | | |
| | cDNA Library Preparation: Life Technologies, Inc. | | |
| | CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) | | |
| | DNA Sequencing by: Incyte Genomics, Inc. | | |
| | Clone distribution: MGC clone distribution information can be | | |
| | found through the I.M.A.G.E. Consortium/LNL at: | | |
| | http://image.lnl.gov | | |
| | Plate: L14M9732 | | |
| | row: d | | |
| | column: 03 | | |
| | High quality sequence stop: 726. | | |
| | location/Qualifiers | | |
| | 1. 858 | | |
| | /organism="Homo sapiens" | | |
| | /db_xref="taxon:9606" | | |
| | /clone="IMAGE:3912914" | | |
| | /clone_id="NIH_MGC_71" | | |

| Query Match | 39.9% | Score 584 | DB 141 | Length 858 |
|-----------------------|---|--------------------|---------------------------------------|-------------|
| Best Local Similarity | 100.0% | Pred. No. 2.3e-275 | | |
| Matches 584 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps |
| | | | | |
| 145 | gaatlatataacccaagaagtcatttgagcaagatgacgctgagatcacttccaagtga | 204 | | |
| 1 | GAATATATTAAACCTCAAAAGTCATTGGACAGGATGACGATGAGATTCACCTCAAGTGAAA | 60 | | |
| 205 | atgacacacatctccaagaagaactcaagaatcattctgccaagacagggtgttccaatg | 264 | | |
| 61 | ATGACAAACACATCTCCAAACAACTCAAAAGAAATCAATGCTCAAAACAGGGGCTCCAAATG | 120 | | |
| 265 | aattcaaccaggttctctctttgaggttcaagagaattctgtatactactccaaga | 324 | | |
| 121 | AATTACACACAGTTTCTCTTTGAGGGTCAGAGAAATGCTGATATCATCTCCAAAAGAA | 180 | | |
| 325 | ctgaggaatgagaggaagaagatgcatgaaagtltatcaagaaacaacgggggtcaltca | 384 | | |
| 181 | CTGGCAATGAGAGAAAGAGATGATTCGAATTCGAATTCATCAGCAACAAACGGGGGTCATTTC | 240 | | |
| 385 | acaatttatgatactctttatctttttttcttccctcccaactccttttattttaa | 444 | | |
| 241 | ACAGTTTGAATATCTTTTATTTTATTTTCTTTTCCCTCAATCCTTTTATTTTAAAA | 300 | | |
| 445 | atagttctcttgaatgctgctgttcaaaacggaattgaaactgacaccatctcttg | 504 | | |
| 301 | ATAGTTCTTTTGTAAATGAGTGCTTCAAAACGGAATGAAACCTGGACCCCATCTCTTG | 360 | | |
| 505 | aaacatctggttaatttgatctctatgctcatctattcatattgtttgtttcatgtgc | 564 | | |
| 361 | AAACATCTGCGTAATTTGTAATCTCTGATGCTCATTTATTTATTTATTTTGTTCATTTGTC | 420 | | |
| 565 | tgaatttggatgaatgaagcccaatccctcatatcataaccctccctttaaanaat | 624 | | |
| 421 | TGATTTTGGGATCAACACCTCAGTCCCTTCATATTAACCTCCTTTTAAAAATTAC | 480 | | |
| 625 | gtctgacagagaggtcaaccttttccaggaattgcaatttcagggtctgtgtgataat | 684 | | |
| 481 | GTCGTCACAGAGAGTCACTTTTTCAGGAACTTGCAATTTTCAGGCTTGCTGCTATTAAT | 540 | | |
| 685 | aagatcgacgaatcgaaagtctctcaatgaatgaacttccaatgagcc | 728 | | |
| 541 | AAGATCGACCAATGCAAGTGTTCATTAATGACTTTCACATTTG6CC | 584 | | |
| RESULT 9 | | | | |
| BE889687 | 830 bp | mrna | EST | 20-OCT-2000 |
| LOCUS | 605127718P1 | NIH_MGC_71 | Homo sapiens cDNA clone IMAGE:3914045 | 5', |
| DEFINITION | mrna sequence. | | | |
| ACCESSION | BE889687 | | | |
| VERSION | BE889687.1 | GI:10347260 | | |
| KEYWORDS | EST. | | | |
| SOURCE | human. | | | |
| ORGANISM | Homo sapiens | | | |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| AUTHORS | Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. | | | |
| TITLE | NIH-MGC http://mgc.nci.nih.gov/. | | | |
| JOURNAL | National Institutes of Health, Mammalian Gene Collection (MGC) | | | |
| COMMENT | Unpublished (1999) | | | |
| | Contact: Robert Strausberg, Ph.D. | | | |
| | Email: gga@pds-remail.nih.gov | | | |
| | Tissue Procurement: ATCC | | | |

CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9735 row: c column: 06
High quality sequence stop: 692.
Location/Qualifiers
1..830
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3914045"
/clone_1ib="NIH_MGC_71"
/tissue_type="leiomysarcoma"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 215 a 165 c 188 g 262 t
ORIGIN

Query Match 36.7%; Score 538; DB 141; Length 830;
Best Local Similarity 99.8%; Pred. No. 8.5e-253;
Matches 588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 13 gtaaccccgagagaggttcgttaccgagccgctgtgtgagagaccccggt 72
|||
Db 1 gtaaaccccgagagaggttcgttaccgagccgctgtgtgagagaccccggt 60
|||
OY 73 gaacccacgcacatgctgcacagagagacacacacacacacacacacacac 132
|||
Db 61 gaacccacgcacatgctgcacagagagacacacacacacacacacacacac 120
|||
OY 133 aagaagcaagtgatataataactcaactgacagatgacagatgacatgac 192
|||
Db 121 aagaagcaagtgatataataactcaactgacagatgacagatgacatgac 180
|||
OY 193 ttcaacagtaaatgacacacacacacacacacacacacacacacacacac 252
|||
Db 181 ttcaacagtaaatgacacacacacacacacacacacacacacacacacac 240
|||
OY 253 ggtgtccaaatgaatcactcaggttctcttgaaggtcagaaatgctgataat 312
|||
Db 241 ggtgtccaaatgaatcactcaggttctcttgaaggtcagaaatgctgataat 300
|||
OY 313 actccaaaagaactggaatggaagaaagatgataatgataatgataatgata 372
|||
Db 301 actccaaaagaactggaatggaagaaagatgataatgataatgataatgata 360
|||
OY 373 ggggggtcattcaacagttgataatcttttttttttttttttttttttttt 432
|||
Db 361 ggggggtcattcaacagttgataatcttttttttttttttttttttttttt 420
|||
OY 433 ttattttaaaatagttcttcttgaatggtgtcctcaacagaaatgaaatgac 492
|||
Db 421 ttattttaaaatagttcttcttgaatggtgtcctcaacagaaatgaaatgac 480
|||
OY 493 ccaatctcttgaacacatcgtgtaattgaaatcagatcattcattatgtttg 552
|||
Db 481 ccaatctcttgaacacatcgtgtaattgaaatcagatcattcattatgtttg 540
|||
OY 553 ttctcatgtgctgatttttggatgatacagcctcattccctcattt 601
|||
Db 541 ttctcatgtgctgatttttggatgatacagcctcattccctcattt 589
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RESULT 10
BG169405 1166 bp mRNA EST 06-FEB-2001
LOCUS BG169405 602320976F1 NIH_MGC_89 Homo sapiens cDNA IMAGE:4424131 5',
DEFINITION mRNA sequence.

ACCESSION BG169405
VERSION BG169405.1 GI:12676108
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE NIH-MGC http://imgc.ncl.nih.gov/
1 (bases 1 to 1166)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL).
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10167 row: h column: 20
High quality sequence stop: 672.
Location/Qualifiers
1..1166
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4424131"
/clone_1ib="NIH_MGC_89"
/tissue_type="hypernephroma, cell line"
/note="Organ: kidney; Vector: PCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

BASE COUNT 368 a 197 c 282 g 318 t 1 others
ORIGIN

Query Match 35.8%; Score 524; DB 174; Length 1166;
Best Local Similarity 99.6%; Pred. No. 6.3e-246;
Matches 674; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 gaaggggttgaaccccgagagaggttcgttaccgagccgctgtgagaga 63
|||
Db 2 gaaggggttgaaccccgagagaggttcgttaccgagccgctgtgagaga 61
|||
OY 64 ccccggttgaaccccgagagaggttcgttaccgagccgctgtgagaga 123
|||
Db 62 ccccggttgaaccccgagagaggttcgttaccgagccgctgtgagaga 121
|||
OY 124 ttgggggataagaagcaagtgataatataactcaaatgataatgataatgata 183
|||
Db 122 ttgggggataagaagcaagtgataatataactcaaatgataatgataatgata 181
|||
OY 184 gaattcacttcaaatgataatgataatgataatgataatgataatgataatgata 243
|||
Db 182 gaattcacttcaaatgataatgataatgataatgataatgataatgataatgata 241
|||
OY 244 caaagcaggtgttccaatgataatgataatgataatgataatgataatgata 303
|||
Db 242 caaagcaggtgttccaatgataatgataatgataatgataatgataatgata 301
|||
OY 304 gataatcacttcaaatgataatgataatgataatgataatgataatgataatgata 363
|||
Db 302 gataatcacttcaaatgataatgataatgataatgataatgataatgataatgata 361
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OY 364 gaacaaaggggtcattcaacagttgataatgataatgataatgataatgataatgata 423
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Db 362 gaacaaaggggtcattcaacagttgataatgataatgataatgataatgataatgata 421
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OY 424 aatccttttattttttaaaatagttcttcttgaatggtgtgttcaaaagaaatgaa 483
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Db 422 AACCTTTTATTTTAAAAATAGTCTTTTGTATGATGCTGTTCAAAACGGAATTGAA 481
Qy 484 aacggagacccatctcttgaacatctgtaattgaattcagaagtcattatcat 543
Db 482 AACTGGACCCCATCTCTTGAACATCTGTAATTGAAATTCATGATTCATTTATTCAT 541
Qy 544 tatgtctgttctatctgctgtaatttgggtgatacgaagccctcagtcctcattac 603
Db 542 TATGTTGCTTTCATGATGCTGATTTGGGTGATCAAGCTCAGTCCCTTCATATTAC 601
Qy 604 cctctcttctttaaataatcagtgacagagagtgacacttcttcaagcattgatt 663
Db 602 CCTCTCTTTTAAAAATAGTCTGTCACAGAGAGTCACTTTTCAAGCAATTGCAATT 661
Qy 664 ttcagctgtgtgtgat 680
Db 662 TTCAGGCTGTGTGAT 678

RESULT 11
LOCUS AV718177 698 bp mRNA EST 16-OCT-2000
DEFINITION AV718177 FHFA Homo sapiens cDNA clone FHFAAH02 5', mRNA sequence.
ACCESSION AV718177
VERSION AV718177.1 GI:10815329
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 698)
AUTHORS Xiao,H., Peng,Y., Song,H., Gu,Y., Yang,Y., Gao,G., Xu,X., Li,N.,
          Qian,B., Liu,F., Qu,Z., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S., Gu
          ,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Chen,Z. and Han
          ,Z.
          Homo sapiens cDNA FHFA clones
          Unpublished (2000)
          Contact: Zequang Han
          Chinese National Human Genome Center at Shanghai
          351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
          201203, P. R. China
          Tel: 86-21-50801919(ex.45)
          Fax: 86-21-50801922
          Email: hanzg@chgc.sh.cn
          This clone is available at CHGC in Shanghai.
FEATURES
    source
        1. 698
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone_id="FHFAAH02"
            /tissue_type="hypothalamus"
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            /lab_host="BM25.8"
            /note="Vector: pTRIPlex2; Site_1: sf1A; Site_2: sf1B1"

BASE COUNT 201 a 127 c 155 g 213 t 2 others
ORIGIN
Query Match 34.1%; Score 500; DB 32; Length 698;
Best Local Similarity 99.8%; Pred. No. 3,7e-234;
Matches 550; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 128 ACTTGGGGGATAGAGAGAGGTATATATTAACCTCAAGTCAATTGGACAGATAGCA 187
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Db 188 GTGAGATTCACTTAAAGTGAATGACACACATCTCAAGAAACTCAAGAAATCAATAC 247
Qy 242 gtcaaaagacaggtgtcccaatgaatcaactcaggtctcttggagggtcagaattg 301
Db 248 GTCAAGACAGAGGTGTTCCATGAAATTCACACAGTTCCTTTGAGAGGTGCAGAAATTG 307
Qy 302 ctgatactatctccaaagaactggaaatggagggaagagatgtaattgaattatc 361
Db 308 CTGATTAATCAATCTCAAAAGAACTGGAAATGAGAGAAAGATGATGATTAAGTTATTC 367
Qy 362 aggaacaacaggggggtcatcacaacagtttagatattcttcttcttcttcc 421
Db 368 AGGAACAAGAGGGGGGTGATTCACACAGTTATGATTTCTTTATTTTCTTTCC 427
Qy 422 tcaatccttttattttaaataagttcttggtaatgtgtgtgttcaaaaggaattg 481
Db 428 TCAATCTTTTATTTTAAAAATAGTCTTTGTATGTGTGTTCAAAACGGAATTG 487
Qy 482 aaacgtgaccccatctcttgaacatctggtgaattgaattcagtgctcatatc 541
Db 488 AAAACTGGACCCCATCTCTTGAACATCTGTGTAATTGTAATCTAGTCTATATTC 547
Qy 542 atattgttg 552
Db 548 ATTAATTGTTG 558

RESULT 12
LOCUS BG399175 850 bp mRNA EST 12-MAR-2001
DEFINITION BG399175 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4556534 5',
ACCESSION BG399175
VERSION BG399175
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC http://mgc.ncl.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
          Email: cgabs-remail.nih.gov
          Tissue Procurement: CLONTECH Laboratories, Inc.
          cDNA Library Preparation: CLONTECH Laboratories, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLB)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clona distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNLB at:
          http://image.llnl.gov
          Plate: LCM1259 row: e column: 15
          High quality sequence stop: 673.
FEATURES
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        1. 850
            /organism="Homo sapiens"
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            /clone_id="IMAGE:4556534"
            /clone_1lb="NIH_MGC_75"
            /lab_host="DH10B (TI phage-resistant)"
            /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
            /sf1 (ggccgcctggcc); Site_2: Sf11 (ggccatattggcc); 5' and
            3' adaptors were used in cloning as follows: 5' adaptor
            sequence: 5'-CACGGCCATTAATGGC-3' and 3' adaptor sequence:
            5'-ATTCTAGAGCCGAGGCGCCGAGATG-dT(30)BN-3' (where B = A,
            C, or G and N = A, C, G, or T). Average insert size 1.65
            kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
            by PCR. This library was enriched for full-length clones

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Best Local Similarity 99.4%; Pred. No. 1,1e-231;
Matches 695; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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OY 4 gaagatttgaaccccgagaggttcttaccgagccgctgctgctgagaga 63
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DB 19 GAAGATTGTGAACCCGAGCGGAGGTTGCTTACCCGAGCGCGTGTGGGAGA 78
OY 64 ccccggttgaagccacgcatcatgtctgaccagaggaacccctcaactgaagac 123
    |||||||
DB 79 CCCCCGGTGAAGCCGTCATGTCTGACCAAGAGGCAAAACCTTCAACTGAGGAC 138
OY 124 ttggggtaagaagcaagtgaatataataactcaaatgcaatggagatagcagt 183
    |||||||
DB 139 TTGGGGTAAGAAGAGAGTGAATATATTAACCTCAAGTCATTGGACAGATAGCAGT 198
OY 184 gagatccttcaaatgaataatgacaacacatctcaagaactcaagaatcatactgt 243
    |||||||
DB 199 GAGATTCACTTCAAAATGAATGACAACACATCTCAAGAACTCAAGATCATCTGT 258
OY 244 caaagacagaggtgttccaatgaatcaactcaggttctcttggaggtcagagaattgct 303
    |||||||
DB 259 CAAAGACAGGGGTGTTCCATGATTCATCTCAGGTTCTCTTGGAGGTCAGAGATTGCT 318
OY 304 gataatcaactccaagaactggaatggaagagaagatgtgattgaagttatcag 363
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DB 319 GATATATCACTCCAAAAGAACTGGGAATGAGAGAAAGATGATGAAATTGATTCAG 378
OY 364 gaacaaacggggggttcaatcaagttagaatcttatttttttttttttttttttt 423
    |||||||
DB 379 GAACAAACGGGGGTCATTCAACAGTTAGATATCTTTTATTTTCTTTTCCCTC 438
OY 424 aatccttttatttttaaaaaatagttccttcttgaatggtgttcaaaacggaattgaa 483
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DB 439 AATCCTTTTATTATTTTAAATAATAGTTCTTTGTAATGTGTTCAAAACGAATTGAA 498
OY 484 aactggaccccccatctcttgaacaatctggttaattgaattcagtgctcatatcat 543
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DB 499 AACTGGCACCCCATCTCTTGAACATCTGTGAATTGAAATTCATGCTCATATTTCAT 558
OY 544 tatgttgttcatatgtgtgatttttttttttttttttttttttttttttttttttt 603
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DB 559 TATGTTTGTGTTTCAATGTGTCTGATCCTTGTGATCAAGCCTCAGTCCCTTCATATTAC 618
OY 604 cctctccttttaaaaaatlaacgtgtgacagagagtcaccttttcaagacattgcat 663
    |||||||
DB 619 CCTCTCCTTTTAAATAATAGTGTGACACAGAGAGTCACTTTTCAGAGCATTTGCATT 678
OY 664 ttcaaggtctgtgtgataaataagatcgaccaatgcag 702
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DB 679 TTCAGGCTTGTGTGATTAATTAAGATGACCAATGCAAG 717
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Job time: 4517 sec

